

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 13:34:52 ; Search time 115 Seconds
(without alignments)
2509.343 Million cell updates/sec

Title: US-09-623-514A-2

Perfect score: 2771

Sequence: 1 MAILDSAGVTIVTNGGEF.....OPMCVLLYYHLMKRGKMS 520

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1355418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QWMT=fastap -SUP=ix=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2771	100.0	1942	US-09-326-203A-1	Sequence 1, Appli
2	2309.5	83.3	1512	US-09-593-359-3	Sequence 3, Appli
3	1833	66.1	1446	US-09-593-359-1	Sequence 1, Appli
4	794	28.7	1976	US-09-165-042-2	Sequence 2, Appli
5	773.5	27.9	1650	US-09-103-754A-2	Sequence 2, Appli
6	773.5	27.9	1766	US-09-326-203A-15	Sequence 15, Appli
7	773.5	27.9	1766	US-09-326-203A-16	Sequence 16, Appli
8	709.5	25.6	1895	US-09-326-203A-14	Sequence 14, Appli
9	652.5	23.5	629	US-09-103-754A-3	Sequence 3, Appli
10	412.5	14.9	4011	US-08-121-057-3	Sequence 3, Appli
11	412.5	14.9	4011	US-08-509-187D-3	Sequence 3, Appli
12	412.5	14.9	4011	US-09-121-396-3	Sequence 3, Appli

13	412.5	14.9	4011	5	PCT-US93-09704A-3	Sequence 3, Appli
14	405.5	14.6	4079	1	US-08-121-057-2	Sequence 2, Appli
15	405.5	14.6	4079	2	US-08-509-187D-2	Sequence 2, Appli
16	405.5	14.6	4079	2	US-09-121-396-2	Sequence 2, Appli
17	405.5	14.6	4079	5	PCT-US93-09704A-2	Sequence 2, Appli
18	375	13.5	1607	4	US-09-328-857A-1	Sequence 2, Appli
19	364.5	13.2	1509	4	US-09-328-857A-2	Sequence 2, Appli
20	364	13.1	2040	3	US-09-165-042-4	Sequence 4, Appli
21	299	10.8	275	4	US-09-326-203A-5	Sequence 5, Appli
22	284.5	10.3	253	4	US-09-326-203A-7	Sequence 7, Appli
23	284	10.2	234	4	US-09-326-203A-3	Sequence 3, Appli
24	277	10.0	267	4	US-09-326-203A-4	Sequence 4, Appli
25	275	9.9	254	4	US-09-326-203A-8	Sequence 8, Appli
26	275	9.9	254	4	US-09-313-294A-583	Sequence 583, App
27	266	9.6	262	4	US-09-326-203A-9	Sequence 9, Appli
28	266	9.6	262	4	US-09-313-294A-1562	Sequence 1562, Ap
29	224.5	8.1	518	4	US-09-326-203A-12	Sequence 12, Appli
30	187.5	6.8	519	4	US-09-326-203A-11	Sequence 11, Appli
31	166.5	6.0	325	4	US-09-326-203A-10	Sequence 10, Appli
32	151	5.4	996	1	US-08-121-057-1	Sequence 1, Appli
33	151	5.4	996	2	US-08-509-187D-1	Sequence 1, Appli
34	151	5.4	996	2	US-09-121-396-1	Sequence 1, Appli
35	151	5.4	996	5	PCT-US93-09704A-1	Sequence 1, Appli
36	150	5.4	6755	3	US-08-931-999-4	Sequence 4, Appli
37	144	5.2	1239	4	US-09-134-001C-2548	Sequence 2048, Ap
38	142.5	5.1	3967	4	US-09-672-743-14	Sequence 14, Appli
39	141.5	5.1	92407	4	US-09-596-002-36	Sequence 36, Appli
40	132.5	4.8	1500	4	US-09-540-236-1237	Sequence 1297, Ap
41	130	4.7	1218	4	US-09-134-000C-2067	Sequence 2067, Ap
42	122.5	4.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
43	120	4.3	3707	1	US-08-118-101A-1	Sequence 1, Appli
44	117	4.2	7557	1	US-08-464-136-4	Sequence 4, Appli
45	117	4.2	7557	2	US-08-349-131-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-326-203A-1
; Sequence 1, Application US/09326203A
; Patent No. 644876
; GENERAL INFORMATION:

; APPLICANT: Lasser, Mike
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/109,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1942
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-326-203A-1

Alignment Scores:
Pred. No.: 4.71e-296 Length: 1942
Score: 2771.00 Matches: 520
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-623-514A-2 (1-523) x US-09-326-203A-1 (1-1942)

Qy 1 MetAlaileLeuAspSerAlaGlyValThrValThrGluAsnGlyGlyGluPhe 20

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60 ArgAspArgIleAspSerValValAsnAspAlaGlnGlyThrAlaAsnLeuAlaGly 79
160 AGGATCGGTTGATTCGCTCGCGAGGAGGAGCTCAGGGAACAGCGAATTAGCT--- 216
80 AspAsnAspGlyGlyGlyAspAsnAsnGlyGlyGlyArgGlyGlyGlyGlyGly 99
217 -----GGCGGAGATCGCGAATAAGGAATCCGCGGAGGC----- 252
100 AsnAlaAspAlaThrPheThrThrArgProSerValProAlaHisArgArgAlaArgGlu 119
253 -----GATG-AAGCTTACGTAACGCTCGGTTCCAGCTCAACGGAGACGAGGAG 306
120 SerProLeuSerSerAspAlaIlePheLysGlnSerHisAlaGlyLeuPheAsnLeuCys 139
307 AGTCTCTCAGCTCCGACGCTATCTTCAACAAAGCCATGACAGGATGTTCAACCTCTGT 366
140 ValValValLeuLeuAlaValAsnSerArgLeuLeuLeuLeuLeuLeuLeuLeuLeu 159
367 GTAGTTGTTCTTGTGCTGTTAAACAGTAGACTCATCATCGAAACCTCATGAAGTATGT 426
160 TrpLeuIleArgThrAspPheThrPheSerSerArgSerLeuArgAspTrpProLeuPhe 179
427 TGGTTGATCAGAACTGATTTTGTGTTAGTTTCTACATCTTACGAGACTGCGCGCTTTC 486
180 MetCysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGluLysLeuVal 199
487 ATGTTGTTCTTACTTTCGCTCTTCTTGGTGTCTTACCGTTCGAGAAATGTGA 546
200 LeuGlnLysIleSerGluProValValIlePheLeuHisIleIleIleThrMetThr 219
547 CTTCAGAAATTCATATCTGAGCTCTGCCATCATCTTCATGTCATTATAACCAATGACA 606
220 GluValLeuIleValProValValThrLeuArgCysAspSerAlaPheLeuSerGlyVal 239
607 GAGTCTTGTATCCAGTCTACGTCACCTGAGTGTGATTCGCTTCTTGTGACGGTGC 666
240 ThrLeuMetLeuLeuThrCysIleValTrpLeuLysLeuValSerTyrAlaHisThrSer 259
667 ACCTTGAGCTGCTCCTTGCATTTGTTGGCTGAAGTTGGTTTCTACGCTCTACTAGC 726
260 TyrAspIleArgSerLeuAlaAsnAlaAlaAspLysAlaAsnProGluValSerTyrTyr 279
727 TACGACATAGAACCTCGCCAAATTCAGCTGATAGGTCGATCTCGAAATCTCTACTAT 786
280 ValSerLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSer 299
787 GTTAGCTTGAAGAGCTTGGCGTATTTCATGGTTGCTCCACACTGTGTATCAGCCAAAC 846
300 TyrProArgSerAlaCysIleArgCysGlyTrpValAlaArgGlnPheAlaLysLeuVal 319
847 TATCCAGTTCTCCATGATATCCGAGAGGTTGGTGGCTCGCTCACTTGCANAACTGGTC 906
320 IlePheThrGlyPheMetGlyPheIleLeuGlnIleLeuAsnProIleValArgAsn 339
937 ATATTCACTGGACTCATGGATTTATATAGACCAATATATAATCTTATTAGGAAC 966
340 SerLysHisProLeuLysGlyAspLeuLeuTyrAlaIleGluArgValLeuLysLeuSer 359
967 TCAAGACATCTCTGAAAGGGGACCTTCTATATGCTATATGAAGAGTGTGAAGCTTTCA 1026
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1027 GTTCCAAATCTATATGTGGCTCTGATGTTCTACTGCTTCTTCCACCTTTGGTTAAAC 1086
380 IleLeuAlaGluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAla 399
1087 ATATTGGCAGAGCTCTCTGCTTCTGGGACCGCTGAATTTCTACAAAGATTGGTGAATGCA 1146
400 LysSerValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArg 419
1147 AAAAGCGTTGGAGATTATTGGAGAAATGTGAATATATGCTGTTTACAAATGGATGTGCA 1206

QY 420 HisIleTyrPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAla 439
DB 1207 CATGTATACTTTCGCTGCTCGGCTCAAGTACCAAAAGTACCCGCAATATATGCT 1266
QY 440 PheLeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLys 459
DB 1267 TTTCTAGTCTCTGAGCTTTTCATGAGTTATGATCGCAGTTCCTTGGCGTCTCTTCAAT 1326
QY 460 LeuTrpAlaPheLeuGlyIleMetPheGlnValProLeuValPheIleThrAsnTyrLeu 479
DB 1327 CTATCGGCTTTCATGGAAATATGTTTTCAGGTCCTTTCGTTCTTATCAAACTTTTA 1386
QY 480 GlnGluArgPheGlySerThrValGlyAsnMetIlePheTrpPheIlePheCysIlePhe 499
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QY 500 GlyGlnProMetCysValLeuLeuTyrTyrHisAspLeuMetAsnArgLysGlySerMet 519
DB 1447 GGACAAACGATGTGGGCTTCTTATTACCATGACCTGATGAACCGCAAGGATCCATG 1506
QY 520 Ser 520
DB 1507 TCC 1509
RESULT 3
US-09-593-359-1
Sequence 1, Application US/09593359
Patent No. 6552250
GENERAL INFORMATION:
APPLICANT: Laroche, Andre J.
APPLICANT: Nykiforuk, Cory L.
APPLICANT: Weselake, Randall J.
TITLE OF INVENTION: Diacylglycerol O-acyltransferase
FILE REFERENCE: 24015050
CURRENT APPLICATION NUMBER: US/09/593,359
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1446
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
OTHER INFORMATION: DGAT2
NAME/KEY: CDS
LOCATION: (82)..(1107)
US-09-593-359-1
Alignment Scores:
Pred. No.: 1,44e-192 Length: 1446
Score: 1833.00 Matches: 342
Percent Similarity: 95.55% Conservative: 10
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Query Match: 66.15% Indels: 1
DB: 4 Gaps: 0
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QY 173 LeuArgAspTrpProLeuPheMetCysCysIleSerLeuSerIlePheProLeuAlaAla 192
DB 62 CTGGCAGATGTC-CCGCTTTTCATGTTGTGTTCTCCCTTCAATCTCTTCTGGCTGCC 120
QY 193 PheThrValGluLysLeuValLeuGlnLysTyrIleSerGluProValValIlePheLeu 212
DB 121 TTTACCGTCGAGAAATAGTACTTCAAGAAATCAATATCTGAACCTGTTGTCATCTTCT 180
QY 213 HisIleIleIleThrMetThrGluValLeuTyrProValTyrValThrLeuArgCysAsp 232


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Db      820 GGGCTCCCTGCTGGGCTGATGGGCGACACCATCTCTCTCTCAAGCTCTTCTCTACCG 879
Qy      256 aHisThrSerTyrAspIleArgSer-----LeuAlaAsnAl 268
Db      880 C-----GACGTCAACTCATGTGTGCGCAGGGGCCAGGGCCAAAGGCTGCTCTGC 927
Qy      268 aAlaAspLysAlaAsnPro-----GluValSerTyr-----TyrValSe 281
Db      928 AGGAAGAGGCGCAGCATGCTGTGCGCCGCGACACCGTGAGCTACCGGACATCTGAC 987
Qy      281 rLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyrPr 301
Db      988 CTACCGCATCTCTACTACTCTCTCTGCGCCCGACCTGTCTAGAGCTCAACTTCC 1047
Qy      301 cArgSerAlaCysIleArgLysGlyTyrPheValAlaArgGlnPheAlaLysLeuValIlePh 321
Db      1048 CCGCTCTCCCGCATCCGGAGCGCTTCTGTGCGACGATCTTGTGAGATCTGTCTT 1107
Qy      321 eThrGlyPheMetGlyPheIleIleGluGlnTyrIleAenProIleValArgAsnSerly 341
Db      1108 CACCAGCTCAGGCGGGCTGATCCAGCAGGAGGTGCCCCACCATCCAGACTCCAT 1167
Qy      341 sHisProLeuLysGlyAspLeuLeuTyrAla-----IleGluArgValLeuCysLeuSe 359
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Qy      379 nIleLeuAlaGluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTyrTrpAsnAl 399
Db      1285 TGCCGTGCTGAGCTCATGCGATTTGGAGACCGGGAGTCTTACCGGACTGTGTGGACTC 1344
Qy      399 aLysSerValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTyrPheValAr 419
Db      1345 CGAGTCTGTCACTACTCTGCGCAGAACTGGAACATCCCTGTGCAACAGTGTGTCATCAG 1404
Qy      419 gHisLysTyrPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAl 439
Db      1405 ACATCTTACAGCCCATCTTCGACGGGCGAGCAAGTGGATGGTCCGACAGAGGGGT 1464
Qy      439 aPheLeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLy 459
Db      1465 GTTCTGCTGCTCGCTTCTTCCAGAGTACTGTGGAGCGTCCCTCTCGAATGTTCG 1524
Qy      459 sLeuTrpAlaPheLeuGlyIleMetPheGlnValProLeuVal---PheIleThrAsnTy 478
Db      1525 CTTCTGGGCTTTCACGGGCATGATGGCTCAGATCCCATCTGGCTGTGTTCTGGGGCGCTT 1584
Qy      478 rLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePheTrpPheIlePheCysIl 498
Db      1585 TTTCAGGCGCAACTAT-----GGCAACGCGAGCTGTGTGG---CTGTGCTCAT 1629
Qy      498 ePheGlyGlnProMetCysValLeuLeuTyrTyrHisAsp 511
Db      1630 CATCGACAGCCCATAGCGCTCTCATGTATCGTCCACGAC 1669

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RESULT 5

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US-09-103-754A-2
; Sequence 2, Application US/09103754A
; Patent No. 634548

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GENERAL INFORMATION:

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; APPLICANT: Farese, Robert
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-acyltran
; TITLE OF INVENTION: sferase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed
; STREET: 285 Hamilton Avenue, Suite 200

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; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,754A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 6510-105p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650 327 3400
; TELEFAX: 650 327 3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-103-754A-2

Alignment Scores:
Pred. No.: 2,41e-75 Length: 1650
Score: 773.50 Matches: 191
Percent Similarity: 51.81% Conservative: 81
Best Local Similarity: 36.38% Mismatches: 178
Query Match: 27.91% Indels: 75
DB: 4 Gaps: 15

US-09-623-514A-2 (1-520) x US-09-103-754A-2 (1-1650)

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Db      141 GGTCTCGGGTTTCTCCAGGTGTAGTGGCCCAAGGTAGAGAGGACGAGGTGCGA 200
Qy      28 ArgArgLysSerArgSerSerSerAsnGlyLeuLeuLeuSerGlySerAspAsn 47
Db      201 GACGCGCTGTGAGCCCGAC-----TTGGCGCGCGGGGTGACGCGCG 245
Qy      48 SerProSerAspValGlyAlaProAlaAspValArgAspArgIleAspSerValVal 67
Db      246 GCTCCGCGTCCG-----GCTCCAGCCCATACCCGCGACAA----- 281
Qy      68 AsnAspAspAlaGlnGlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyGlyAspAsn 87
Db      281 ----- 281
Qy      88 AsnGlyGlyGlyArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 107
Db      282 ---GACGGCGGACCGACCGCTGGCGCGCGCTACTGGGATCTGAGGTGC----- 326
Qy      108 ArgProSerValProAlaHisArgArgAlaArgGluSerProLeuSerSerAspAlaIle 127
Db      327 -----CATCTCTGCAAGATCTTTGTCTCAGCTCAGACAGGTGT 365
Qy      128 PheLysGlnSerHisAlaGlyLeuPheAsnLeuCysValValValLeuIleAlaValAsn 147
Db      366 TTC---AGCAATTATCTGTTATCTTCAATTGTTGTTGTTGTTGTTGTTGTTGTTGTT 422
Qy      148 SerArgLeuIleIleGluAsnLeuMetLysTyrGlyTyrLeuIleArgThrAspPheTrp 167

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Db 564 CTGCTACAGTGGTTAACTGCGCCACAAATATCTGCTCCAGCAGCTGTGGCTTACTG 523
QY 231 CysAspSerAlaPheLeuSerGlyValThrLeuMetLeuLeuThr---CysIleValTrp 249
Db 624 GTTGAAGTCTATCAGTCCAGTGGTTCCTGTTGTCTGGCATCATCTCCATCATCTTC 583
QY 250 LeuLysLeuValSerTyrAlaHisThrSerTyr-----AspIleArgSer 264
Db 684 CTCAGAGCTTCTCTCCAGCGGATGTCATCTGTGGTCCGCCAGGAAGGGTCAAGGCC 743
QY 265 LeuAlaAsnAlaAspLys-----AlaAsnProGluValSerTyr 278
Db 744 AAAGCTGTCTCTGCGAGGAAGGTCAGTGGGGTGTCTGCCAGAACACTGTGAAGCTAT 803
QY 279 -----TyrValSerLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyr 296
Db 804 CGGCACAACTGACCTTACCAGATCTCTATTATCTTCTGCTCTCTCTTGTGTATTAT 863
QY 297 GlnProSerTyrProArgSerAlaCysIleArgLysGlyTyrValAlaArgGlnPheAla 316
Db 864 GAACCAACTCTCTCGATCCCGAATACGAAGCGCTTTCTGTACGGGGTTCCT 923
QY 317 LysLeuValIlePheThrGlyPheMetGlyPheIleIleGluGlnTyrIleAsnProIle 336
Db 924 GAGATGCTCTTTTCAACCCAGCTTCAAGTGGGGCTGATCCAGCAGTGGATGGTCCCTACT 983
QY 337 ValArgAsnSerLysHisProLeuLysGlyAspLeuLeuTyrAla-----IleGluArg 354
Db 984 ATCCAGAACTCCATGAAGCCCTTCAAG--GACATGGACTATTCAGAAATCATATTGAGCGT 1040
QY 355 ValLeuLysLeuSerValProAsnLeuTyrValThrLeuCysMetPheTyrCysPhePhe 374
Db 1041 CTTCTAAAGCTGGGGTCCCGAACCACTGATGATGGCTCATCTTCTTATTTGGCTTTTC 1100
QY 375 HisLeuTrpLeuAsnIleLeuAlaGluLeuLysPheGlyAspArgGluPheTyrLys 394
Db 1101 CACTCATGTCTCAATGCTGTGGCAGAGCTCTCGAGTTTGGAGACCGCAGTCTACAGG 1160
QY 395 AspTrpTrpAsnAlaLysSerValGlyAspTyrTrpArgMetTrpAsnMetProValHis 414
Db 1161 GACTGGTGAATGCTGAGTCTGTACCTACTTTTGGCAGAACTGGAATATCCCGTGCAC 1220
QY 415 LysTrpMetValArgHisIleTyrPheProCysLeuArgSerLysIleProLysThrLeu 434
Db 1221 AAGTGTGTGTCAGACACCTTCTACAGCCTATGCTCAGACTGGCGCAGCAATATGGATG 1280
QY 435 AlaIleIleIleAlaPheLeuValSerAlaValPheHisGluLeuCysIleAlaValPro 454
Db 1281 GCCAGGACTGGGGTCTTTTGGCGTCAGCCTTCTCCATGAGTACCTAGTACGAGCATCC 1340
QY 455 CysArgLeuPheLysLeuTrpAlaPheLeuGlyIleMetPheGlnValProLeuValPhe 474
Db 1341 CTGAGGATGTCGCGCTCTGGGCAATTCACAGCCATGATGGCTCAGTCCCACTGGCGCTGG 1400
QY 475 IleThrAsnTyrLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePheTrpPhe 494
Db 1401 ATGTGTGAACCGCTTC-----TTCAGAGGAACATATGGCAATGCAGCTGTGTGG--- 1448
QY 495 IlePheCysIlePheGlyGlnProMetCysValLeuLeuTyrTyrHisAsp 511
Db 1449 GTGACACTCATATTTGGGCAACGGTGGTGTGCTCATGTATGTATCCACGAC 1499
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RESULT 8

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US-09-326-203A-14
; Sequence 14, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Lasser, Mike
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/NO
; CURRENT APPLICATION NUMBER: US/09/326,203A
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; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (209)
; OTHER INFORMATION: n at position 209 is unknown
US-09-326-203A-14

Alignment Scores:
Pred. No.: 3 61e-68 Length: 1895
Score: 709.50 Matches: 160
Percent Similarity: 58.72% Conservative: 69
Best Local Similarity: 41.03% Mismatches: 128
Query Match: 25.60% Indels: 33
DB: 4 Gaps: 12

US-09-623-514A-2 (1-520) x US-09-326-203A-14 (1-1895)
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QY 144 IleAlaValAsnSerArgLeuIleIleGluAsnLeuMetLysTyrGlyTrpLeuIleArg 163
Db 234 ATCTTGAGCAATGCCCGGTTATTTCTGGAGAACTCATCAAGTATGGCATCTCTGGTG-- 290
QY 164 ThrAspPheTrpPheSerSerArgSerLeuArgAsp-----TrpProLeuPheMet 180
Db 291 GACCCGCTCAGGTGGTTCTCTGTTCTTGAAGATCCCTATAGCTGGCCGCCCCCATGC 350
QY 181 CysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGluLysLeuValLeu 200
Db 351 CTGTTTATTGGCGCAATGCTTTGTGTGGTGCATTCAGGTTGAGAAGCGCTGGCG 410
QY 201 GlnLysTyrIleSerGluProValIlePheLeuHisIleIleIleThrMetThrGlu 220
Db 411 GTGGGTGCTTCAGCGAGCGCGGAGCTGCTCTGACGTGGCCAACTGGGCCACCAT 470
QY 221 ValLeuTyrProValTyrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThr 240
Db 471 CTGTGTTTCCAGCGGCTGTGGTCTTACTGTGTGAGTCTATCACTCAGTGGGCTCCCTG 530
QY 241 LeuMetLeuLeuThr---CysIleValTrpLeuLysLeuValSerTyrAlaHisThrSer 259
Db 531 CTGGCGCTGATGGCGCACACCATCTCTTCTCAAGCTCTTCTCTACCGC----- 581
QY 260 TyrAspIleArgSer-----LeuAlaAsnAlaAlaAspLys 271
Db 582 ---GAGCTCAACTCATGTGGTCCGCGAGCGGCGAGGCTCCCTCTGAGGAGAGAG 638
QY 272 AlaAsnPro-----GluValSerTyr-----TyrValSerLeuLysSer 284
Db 639 GCCAGCAGTGTGCTGCTCCCGCGACACCGTGAGTACCCGACAACTTGACCTACCGGAT 698
QY 285 LeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAla 304
Db 699 CTCTACTACTTCTCTTCGCCCGCACCTTGTGTACGAGCTCAACTTTCCTCCGCTCTCC 758
QY 305 CysIleArgLysGlyTrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPhe 324
Db 759 CGCATCCGGAAGCGCTTCTGCTGGCAGCGATCCCTTGAGATGCTGTCTTCTACCCAGCTC 818
QY 325 MetGlyPheIleIleGluGlnTyrIleAsnProIleValArgAsnSerLysHisProLeu 344
Db 819 CAGTGGGCTGATCCAGCAGTGGATGGTCCCGACCATCCAGAACTCCATGAAGCCCTTC 878
QY 345 LysGlyAspLeuLeuTyrAla-----IleGluArgValLeuLysLeuSerValProAsn 362
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,057
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1397..3046
; US-08-121-057-3

Alignment Scores:
Pred. No.: 8 56e-35 Length: 4011
Score: 412.50 Matches: 148
Percent Similarity: 42.46% Conserved: 80
Best Local Similarity: 27.56% Mismatches: 173
Query Match: 14.89% Indels: 136
DB: 1 Gaps: 23

US-09-623-514A-2 (1-520) x US-08-121-057-3 (1-4011)

QY 17 GlyGlyGluPheValAspLeuArgArgLysSerArgSerSerSer 36
Db 1604 GGCAGTCACCTTCATGATTTTGTGACCAATCTCATTGAAAGTCAGCATCATAGATAAT 1663
QY 37 AsnGlyLeu-----LeuLeuSerGlySerAspAsnAsnSerProSer 50
Db 1664 GGTGGTGGCGCTCTCACACCTTTCTGTCTCTTGAAGGAGAGAAACCAACCATAGAGCG 1723
QY 51 AspAspValGlyAlaProAlaAspValArgAspArgIleAspSerValValAsnAspAsp 70
Db 1724 AGGATTTGAGACCACTCCAGAA-----1747
QY 71 AlaGlnGlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyGlyAspAsnAsnGlyGly 90
Db 1748 ---CAAGGAAAGATTTTATT-----1765
QY 91 GlyArgGlyGlyGlyGlyGlyArgGlyAsnAlaAspAlaThrPheThrTyrArgProSer 110
Db 1765 -----1765
QY 111 ValProAlaHisArgArgAlaArgGluSerProLeuSerSerAspAlaIlePheLysGln 130
Db 1766 -----GCAAGCGCTCTCTCTTA-----GATGAACCTGCTTGAAGTG 1801
QY 131 SerHis---AlaGlyLeuPheAsnLeuCysValValValLeuIleAla---ValAsnSer 148
Db 1802 GACCACATCAGAACAAATATATCATCTTTATTATGCGCTCTCATCTCTTTATCCTCAGC 1861
QY 149 ArgLeuLeuIleGlu-AsnLeuMetLysTyrGlyTyrLeuIleArgThrAspPheTrp 168
Db 1862 ACACCTTGATGATTAATCATTTGATGAGAGAGCGCTGGTGGTGGT-----1907
QY 168 eSerSerArgSerLeuArg-AspTrpProLeuPheMetCysAspIleSerLeuSer-Ile 187
Db 1908 -TCAGCGCTCTGCTTATGCTTTTGGCAAA-TTCCTACCGTTGTTTGGACCTGGTGGATC 1966
QY 188 PheProLeuAlaAlaPheThrValGluLysLeuLeuGlnLysTyr-----203
Db 1967 ATGTTCTCTGTACATTTTCAGTTCCCTATTTCTGTCTTCAACATTTGGCGCACTGGCTAT 2026

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QY 204 -----IleSerGluProValValIle-----PheLeuHisIleIleIle 216
Db 2027 AGCAAGAGTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTCTTTTCATGATCTTC 2086
QY 217 ThrMetThrGluValLeuTyr---ProValTyrValThrLeuArgCysAspSerAlaPhe 235
Db 2087 CAGATTGGAGTTCTAGGTTTGGACCAACATATGTTGTTA-----GCATAT 2134
QY 236 LeuSerGlyValThrLeuMetLeuLeuThrCysIleValThrLeuLysLeuValSerTyr 255
Db 2135 ACACGTCACCAAGCTTCCCGTTTCATCATATATATGAGCAGATCTCTTTGTAATGAAG 2194
QY 256 AlaHisThr-----SerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLysAla 272
Db 2195 GCCCACTCATTTTGTGTCAGAGAACGTCGCTGCGTACTTAATTCAGTAGGAGAAATCA 2254
QY 273 Asn-----ProGluValSerTyrTyrValSerLeuLysSerLeuAlaTyrPhe 288
Db 2255 AGCACTGTTCCCAATACCTACAGTCAACCACTATTG-----TACTTC 2296
QY 289 MetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAlaCysIleArgLys 308
Db 2297 TTATTTGCTCTACCTTATCTACCGTCAGAGCTATCCAGGAATCCCACTGTAAGATGG 2356
QY 309 GlyTyrValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIle 328
Db 2357 GGTATGTGCTATGAGTTTGCAGAGTCTTGGTGTCTTTTCTATGTACTACTACTC 2416
QY 329 IleGluGlnTyrIleAsnProIleValArgAsnSerLys---HisProLeuLysGlyAsp 347
Db 2417 TTGMAAGGCTTGTGCGCCCTTGTTCGGAATATCAACAGGAGCGCTTCAGCGCT---2473
QY 348 LeuLeuTyrAlaIleGluArgValLeuLysLeuSerVal-----ProAsn 362
Db 2474 -----CGTTCTGGTCTATGTTGATTTACTCCATCTCCAGGT 2515
QY 363 LeuTyrValTyrLeuCysMetPheTyrCysPhePheHisLeuTyrLeuAsnIleLeuAla 382
Db 2516 GTGCTGATTTCTCTCTTCTTTTTCCTTTTTCGCTGCTGCTCAATGCCTTTGCT 2575
QY 383 GluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAlaLysSerVal 402
Db 2576 CAGATGTTACGCTTTGTGTGACAGATGTTCTATAAGGATTTGTTGAACTCCACGCTAC 2635
QY 403 GlyAspTyrTrpArgMetTyrAsnMetProValHisLysTyrMetValArgHisTyr 422
Db 2636 TCCAACTATATAGAACCTGAAATGTTGTTGCTGCTGCTGCTATATTACTATGCTTAC 2695
QY 423 -----PheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAlaPhe 440
Db 2696 AAGGACTTTCTCTGTTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGTGTCTTT 2755
QY 441 LeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArg-----456
Db 2756 GCTGTATCTGCTGTAGTACAGATATGCTTGGCTGTT---TGCCTGAGCTTTTCTAT 2812
QY 457 -----LeuPheLysLeuTyrAlaPheLeuGlyIleMetPheGlnValProLeuValPhe 474
Db 2813 CCGGTGCTGTGCTGCTCTCATGTTCTTTGGAAATGCTTTCAAC-----TTC 2860
QY 475 IleThrAsnTyrLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePheTrp---493
Db 2861 ATTGTCAATGATAGTCGGAAGAG-----CCGATTTGGAATGTTCTGATGGAGT 2911
QY 494 -----PheIlePheCysIlePheGlyGln 501
Db 2912 TCTCTTTTCTGGCAATGAGGATCTTACTCTGCTTTTATTCTCAA 2956

RESULT 11
US-08-509-187D-3
; Sequence 3, Application US/08509187D
; Patent No. 5834283
; GENERAL INFORMATION:

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QY 457 -----LeuPheLysLeuThrAlaPheLeuGlyIleMetPheGlnValProLeuValPhe 474
 Db 2813 CCGTGTCTGTCTGCTCTTCATGTTCTTTGGAATGCTTTCAAC-----TTC 2860
 QY 475 IleThrAsnThrLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePheTrp--- 493
 Db 2861 ATTGTCAATGATAGTCGAAAG-----CCGATTGGATGTTCTCTGATGTGGACT 2911
 QY 494 -----PheIlePheCysIlePheGlyGln 501
 Db 2912 TCTCTTTCTTGGCAATGGAGCTTACTCTGCTTTTATTCTCA 2956

RESULT 12

US-09-121-396-3

: Sequence 3, Application US/09121396

: Patent No. 5969749

: GENERAL INFORMATION:

: APPLICANT: CHANG, TA-YUEN

: APPLICANT: CHANG, CATHERINE C. Y.

: TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

: TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

: NUMBER OF SEQUENCES: 9

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: LAHIVE & COCKFIELD

: STREET: 28 STATE STREET

: CITY: BOSTON

: STATE: MA

: COUNTRY: USA

: ZIP: 02139

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: ASCII Text

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/121,396

: FILING DATE:

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/509,187

: FILING DATE: 07/31/95

: ATTORNEY/AGENT INFORMATION:

: NAME: LAMPORT HAMMITTE, ANN.

: REGISTRATION NUMBER: 34,858

: REFERENCE/DOCKET NUMBER: DCI-033CPDV

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (617) 227-2700

: TELEFAX: (617) 742-4214

: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 4011 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

US-09-121-396-3

Alignment Scores:

Pred. No.: 8,56e-35 Length: 4011
 Score: 412.50 Matches: 148
 Percent Similarity: 42.46% Conservative: 80
 Best Local Similarity: 27.56% Indels: 136
 Query Match: 14.89% Gaps: 2
 DB:

US-09-623-514A-2 (1-520) x US-09-121-396-3 (1-4011)

QY 17 GlyGlyGluPheValAspLeuAspArgLeuArgArgGlySerArgSerAspSerSer 36
 Db 1604 GGCAGTCACATTGATGATTTTGTGACCAATCTCATTTGAAAAGTCAGCATCATTAGATAAAT 1663
 QY 37 AsnGlyLeu-----LeuLeuSerGlySerAspAsnSerProSer 50

Db 1664 GTGGGGTGGCGCTCTCACACCTTTCTGTCTTGAAGAGAGAAAACACATAGACGG 1723
 QY 51 AspAspValGlyAlaProAlaAspValArgAspArgIleAspSerValValAsnAspAsp 70
 Db 1724 AAGGATTGAGAGCACCTCCAGAA----- 1747
 QY 71 AlaGlnGlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyGlyAspAsnAsnGlyGly 90
 Db 1748 ---CAAGGAAAGATTTTATT----- 1765
 QY 91 GlyArgGlyGlyGlyGluGlyArgGlyAsnAlaAspAlaThrPheThrTyrArgProSer 110
 Db 1765 ----- 1765
 QY 111 ValProAlaHisArgArgAlaArgGluSerProLeuSerSerAspAlaIlePheLysGln 130
 Db 1766 -----GCAAGGCGCTCTCTCTTA-----GATGAACCTGTTGAAGTG 1801
 QY 131 SerHis---AlaGlyLeuPheAsnLeuCysValValValValLeuIleAla---ValAsnSer 148
 Db 1802 GACCACATCAGAACATATATCATGTTTATTCGCCCTCCTCATCTCTTTATCTCTCAGC 1861
 QY 149 ArgLeuIleIleGlu-AsnLeuMetLysTyrGlyTrpLeuIleArgThrAspPheTrpPh 168
 Db 1862 ACCTTGTAGTAGATTACATTGATGAAGAGGCTGGTGTGAGT----- 1907
 QY 168 eSerSerArgSerLeuArg-AspTrpProLeuPheMetCysCysIleSerLeuSer-Ile 187
 Db 1908 -TCAGCTCCTGCTTATGCTTTTGGCAATTTCTACCGTTGTTGGACCTGTGTGGATC 1966
 QY 188 PheProLeuAlaAlaPheThrValGluLysLeuValLeuGlnLysTyr----- 203
 Db 1967 ATGTTCTGCTGTACATTTCAGTTCCCTATTTCTGTTCAACATTTGGCGCAGCTGGCTAT 2026
 QY 204 -----IleSerGluProValValIle-----PheLeuHisIleIleIle 216
 Db 2027 AGCAAGAGTTCTCATCGCTGATCCGTTCTCTCTCCATGCGCTTTCTTTTCATGATCTC 2086
 QY 217 ThrMetThrGluValLeuTyr---ProValTyrValThrLeuArgCysAspSerAlaPhe 235
 Db 2087 CAGATTGGAGTTCTAGGTTTGGACCAACATATGTTGTGTTA-----GCATAT 2134
 QY 236 LeuSerGlyValThrLeuMetLeuLeuThrCysIleValThrLeuLysLeuValSerTyr 255
 Db 2135 ACATGCCACACAGCTTCCCGTTTCATCATTTATTCGAGCAGATCGTTTGTATGAAG 2194
 QY 256 AlaHisThr-----SerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLysAla 272
 Db 2195 GCCCACTATTGTTCAGAGAGAACGTCCTCGGTACTAAATTCAGCTAAGAGAAATCA 2254
 QY 273 Asn-----ProGluValSerTyrTyrValSerLeuLysSerLeuAlaTyrPhe 288
 Db 2255 AGCACTGTTCCAAATACCTACAGTCAACAGATTTTG-----TACTTC 2296
 QY 289 MetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAlaCysIleArgLys 308
 Db 2297 TTATTGCTCTTACCTTATCTACCGTCAGAGCTATCCAGGAATCCCACTGTAGATGG 2356
 QY 309 GlyTrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIle 328
 Db 2357 GGTATGTCGTATGAAGTTTGCACAGTCTTTGTTGTTCTTTTCTATGTCTACTATCATC 2416
 QY 329 IleGluGlnTyrIleAsnProIleValArgAsnSerLys---HisProLeuLysGlyAsp 347
 Db 2417 TTTGAAAGGCTTTGTGCCCTTTGTCGGAATATCAACAGGAGCCCTTCAGCGCT--- 2473
 QY 348 LeuLeuTyrAlaIleGluArgValLeuLysLeuSerVal-----ProAsn 362
 Db 2474 -----CGTTTCTGCTCTATGTGTATTAACTCCATCTTCCAGGT 2515
 QY 363 LeuTyrValTrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnIleLeuAla 382

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Db      2516 GTGCTGATCTCTCTTACTCTTTTTCCTTTTGACCTCGCTGCTCAATGCGCTTTGCT 2575
Qy      383  GluLeuLeuCysPheGlyAspArgGluPheTyrIysAspTrpTrpAsnAlaLysSerVal 402
Db      2576 GAGATGTTAGCTTGTGTGACAGGATGTTCTATAGGATTGGTGAATCCACGCTCATAC 2635
Qy      403  GlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHis-leTyr 422
Db      2636 TCCACATATTAAAGACTGGAATGGTGTGTGCTGATGCTGCTGCTATATATATGCTTAC 2695
Qy      423  -----PheProCysLeuArgSerIysIleProLysThrLeuAlaIleIleAlaPhe 440
Db      2696 AAGGACTTTCTCTGGTTTTCCTCAAGAGATTCAAACTGCTGCTGCTATGTTAGCTGCTTT 2755
Qy      441  LeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArg 456
Db      2756 GCTGTATCTGCTGTAGTACAGGAATATGCTTGGCTGTT--TGCTTGAGCTTTTCTAT 2812
Qy      457  -----LeuPheLysLeuTrpAlaPheLeuGlyIleMetPheGlnValProLeuValPhe 474
Db      2813 CCGTGTCTGTTCGGCTCTTCTATGTTCTTGAATGGCTTTCAAC-----TTC 2860
Qy      475  IleThrAsnTyrLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePheTrp--- 493
Db      2861 ATTGTCAATGATAGTCGGAAGAAG-----CCGATTGGAAATGTTCTGATGGACT 2911
Qy      494  -----PheIlePheCysIlePheGlyGln 501
Db      2912 TCTCTTTTCTTGGCAATGGAGTCTTACTCTGCTTTTATTCTCA 2956

RESULT 13
PCT-US93-09704A-3
; Sequence 3, Application PC/TUS9309704A
; GENERAL INFORMATION:
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
; NUMBER OF SEQUENCES: 9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09704A
; FILING DATE: October 12, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. SER. NO. 959,950
; FILING DATE: October 14, 1992
; APPLICATION NUMBER: U.S. SER. NO. 121,057
; FILING DATE: September 10, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCL-033CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-09704A-3

Alignment Scores:
Pred. No.: 8.56e-35 Length: 4011
Score: 412.50 Matches: 148
Percent Similarity: 42.46% Conservative: 80
Best Local Similarity: 27.56% Mismatches: 173

```

```

Query Match: 14.89% Indels: 136
DB: 5 Gaps: 23
US-09-623-514A-2 (1-520) x PCT-US93-09704A-3 (1-4011)
Qy      17  GlyGlyGluPheValAspLeuAspArgLeuArgArgLysSerArgSerAspSerSer 36
Db      1604 GCGAGTACTTGTGATGATTTTGTGACCAATCTCATTTGAAAGTCAGCATCATTAGATAAT 1663
Qy      37  AsnGlyLeu-----LeuLeuSerGlySerAspAsnAsnSerProSer 50
Db      1664 GGTGGTGGCTCTCACCAACCTTTTCTGTCTTCTGAAGGAGAGAAACCAACCATAGAGCG 1723
Qy      51  AspAspValGlyAlaProAlaAspValArgAspArgLysSerValValAspAsp 70
Db      1724 AAGGATTGTGAGACACCTCCAGAA----- 1747
Qy      71  AlaGlnGlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyAspAsnAsnGlyGly 90
Db      1748 ---CAAGGAAGATTTTATT----- 1765
Qy      91  GlyArgGlyGlyGlyGluGlyArgGlyAsnAlaAspAlaThrPheThrTyrArgProSer 110
Db      1765 ----- 1765
Qy      111 ValProAlaHisArgArgAlaArgGluSerProLeuSerSerAspAlaIlePheLysGln 130
Db      1766 -----GCAAGGCGCTCTCTCTTA-----GATGAACCTGTTGAAGTG 1801
Qy      131 SerHis---AlaGlyLeuPheAsnLeuCysValValLeuIleAla---ValAsnSer 148
Db      1802 GACCATCATCAGAACAAATATATACATGTTATTGCGCCCTCTCATCTCTTATCTCTCASC 1861
Qy      143 ArgLeuIleIleGlu-AsnLeuMetLysTyrGlyTrpLeuIleArgThrAspPheTrpH 168
Db      1862 ACACCTGTGTAGTAGATTACATTGATGAAGGAGCGCTGGTCTTGAGT----- 1907
Qy      168 eSerSerArgSerLeuArg-AspTrpProLeuPheMetCysCysIleSerLeuSer-Ile 187
Db      1908 -TCAGCCCTCTCTTATGCTTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATC 1966
Qy      188 PheProLeuAlaAlaPheThrValGluLysLeuValLeuGlnLysTyr----- 203
Db      1967 ATGTTCTCTGTCTACATTTTCAGTTCCTATTTTCTGTTTCAACATTTGGCGCAGCTAT 2026
Qy      204 -----IleSerGluProValValIle-----PheLeuHisIleIleIle 216
Db      2027 AGCAAGAGTTCTCATCGCTGATCGTTCCTCTCTTCCATGGCTTTCTTTTCATGATCTTC 2086
Qy      217 ThrMetThrGluValLeuTyr---ProValTyrValThrLeuArgCysAspSerAlaPhe 235
Db      2087 CAGATTGAGTTCTTAGGTTTGGACCAACATATGTTGTGTTA-----GCATAT 2134
Qy      236 LeuSerGlyValThrLeuMetLeuLeuThrCysIleValTrpLeuLysLeuValSerTyr 255
Db      2135 ACACCTGCCACAGCTTCCGGTTTCATATTATTTCGACGACATCGTTTGTATGAAG 2194
Qy      256 AlaHisThr-----SerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLysAla 272
Db      2195 GCCCACTCATTTGTGACAGAGAACGTCCTCGGTACTAAATTCAGTAAAGGAGAATCA 2254
Qy      273 Asn-----ProGluValSerTyrTyrValSerLeuLysSerLeuAlaTyrPhe 288
Db      2255 AGCACTGTTCCAAATACCTACAGTCAACCATATTTG-----TACTTC 2296
Qy      289 MetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAlaCysIleArgLys 308
Db      2297 TTTTGTCTCTACCTTATCTACCGTGACACTATCCAGGAATCCCACTGTAAGATCG 2356
Qy      309 GlyTrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIle 328
Db      2357 GGTATGTCGCTATGAAGTTTGCACAGGTCCTTTGTTGCTTTTCTATGTACTACATC 2416

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QY 329 IleGluGlnTyrIleAsnProIleValArgAsnSerLys---HisProLeuLysGlyAsp 347
DB 2417 TTTGAAGGCTTTGGCCCTTGTCTCGGAATATCAAAACAGAGCCCTTCAGCGCT--- 2473
QY 348 LeuLeuTyrAlaIleValArgValLeuLysLeuSerVal-----ProAsn 362
DB 2474 -----CGTGTCTGGTCCCTATGTATTAACCTCCATCTGCCAGGT 2515
QY 363 LeuTyrValTrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnLeuAla 382
DB 2516 GTGCTGATCTCTTCCTACTTTTGTGCTTTTGTGCTGCTGCTGCTCAATGCTTTGCT 2575
QY 383 GluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAlaLysSerVal 402
DB 2576 GAGATGTTACGCTTTGGTGACAGGAGTTCTATAAGGATGGTGGAACTCCACGTCATAC 2635
QY 403 GlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHisIleTyr 422
DB 2636 TCCCACTATATAGAACCTGGATGGTGGTGGTCCATGCTGCTATATTACTATGCTTAC 2695
QY 423 -----PheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAlaPhe 440
DB 2696 RAGGACTTCTCTGGTTTCTCCAGAGATTCAAAATCTGCTGCCATGTAGCTGCTTT 2755
QY 441 LeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArg----- 456
DB 2756 GCTGATCTGCTGTAGTACAGAAATATGCTTGGCTGTT---TGCTGAGCTTTTCTAT 2812
QY 457 -----LeuPheLysLeuTrpAlaPheLeuGluGlyIleMetPheGlnValProLeuValPhe 474
DB 2813 CCGGCTGCTTGGCTCTCTTCATGTTCTTGGAAATGGCTTCAAC-----TTC 2860
QY 475 IleThrAsnTyrLeuGluGluArgPheGlySerThrValGlyAsnMetIlePheTrp--- 493
DB 2861 ATTGCAATGATAGTCGAAAAG-----CCGATTGGAAATGTTCTGATGGACT 2911
QY 494 -----PheIlePheCysIlePheGlyGln 501
DB 2912 TCTCTTCTTGGGCAATGGAGTCTTACTCTGCTTTTATTTCTGAA 2956

RESULT 14
US-08-121-057-2
; Sequence 2, Application US/08121057
; Patent No. 5484727
; GENERAL INFORMATION:
; APPLICANT: CHANG, TA-YUAN
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,057
; FILING DATE:
; CLASSIFICATION: 850
; ATTORNEY/AGENT INFORMATION:
; NAME: LAMPORT HAMMITTE, ANN.
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-2700
; TELEFAX: (617) 227-5941
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-121-057-2

Alignment Scores:
Pred. No.: 5,23e-34 Length: 4079
Score: 405.50 Matches: 148
Percent Similarity: 41.36% Conservative: 77
Best Local Similarity: 27.21% Mismatches: 167
Query Match: 14.63% Indels: 153
DB: 1 Gaps: 24

US-09-623-514A-2 (1-520) x US-08-121-057-2 (1-4079)

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QY 51 AspAspValGlyAlaProAlaAspValArgAspArgIleAspSerValValAsnAspAsp 70
DB 1795 AAGGATTTGAGAGCACCTCCAGAA----- 1818
QY 71 AlaGlnGlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyCysAspAsnAsnGlyGly 90
DB 1819 ---CAAGGAAAGATTTTATT----- 1836
QY 91 GlyArgGlyGlyGlyGluGlyArgGlyAsnAlaAspAlaThrPheThrTyrArgProSer 110
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QY 111 ValProAlaHisArgArgAlaArgGluSerProLeuSerSerAspAlaIlePheLysGln 130
DB 1837 -----GCAAGGCGCTCTCTCTTA-----GATGAACCTGCTTGAAGTG 1872
QY 131 SerHis---AlaGlyLeuPheAsnLeuCysValValValLeuIleAla---ValAsnSer 148
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QY 149 ArgLeuIleIleGlu-AsnLeuMetLysTyrGlyTrpLeuIleArgThrAspPheTrpPh 168
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QY 188 eProLeuAlaAlaPheThrValGluLysLeuValLeuGlnLysTyrIleSerGluProva 208
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Qy 268 -----AlaAlaAspLysAlaAsn-----ProGluValSerTyrTyrVa 280
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Qy 280 LseLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTy 300
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Qy 300 rProArgSerAlaCysIleArgLysGlyTyrValAlaArgGlnPheAlaLysLeuValI 320
Db 2400 TCCAGGAATCCCACTGTAAGATGGGTATGCTTGTCTATGAAGTTGCACAGGTCTTTGG 2459
Qy 320 ePheThrGlyPheMetGlyPheIleLeuGlnTyrIleAsnProIleValArgAsnSe 340
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Qy 414 sLysTrpMetValArgHisIleTyr-----PheProCysLeuArgSerLysIleProLy 432
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Db 2955 GATTTGAAGTTCTGATGAGCTTCTTTCTTGGGCAATGGAGTCTTACTCTGCTT 3014
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RESULT 15

US-08-509-187D-2
; Sequence 2, Application US/08509187D
; Patent No. 5834283
; GENERAL INFORMATION:
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; STREET: LAHIVE & COCKFIELD, LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/509,187D
; FILING DATE: 31-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lamport Hammitte, Ann
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033cpdv
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-509-187D-2
Alignment Scores:
Pred. No.: 5,236-34 Length: 4079
Score: 405.50 Matches: 148
Percent Similarity: 41.36% Conservative: 77
Best Local Similarity: 27.21% Mismatches: 167
Query Match: 14.63% Indels: 153
Gaps: 24
US-09-623-514A-2 (1-520) x US-08-509-187D-2 (1-4079)
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Db 1675 GCGAGTCACTTGATGATTTTGTGACCAATCTCATTGAAAAGTCAGCATCTAGATAT 1734
Qy 37 AsnGlyLeu-----LeuLeuSerGlySerAspAsnAsnSerProSer 50
Db 1735 GGTGGTGGCTCTCACAACTTTTCTGTCTTGAAGGAGAGAAAACAACCATAGAGCG 1794
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Qy 432 sThrLeuAlaIleIleIleAlaPheLeuValSerAlaValPheHisGluLeuCysIleAl 452
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Search completed: May 5, 2004, 20:22:17
Job time : 150 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein: - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 13:34:09 ; Search time 546 Seconds
(without alignments)
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Title: US-09-623-514a-2

Perfect score: 2771

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Searched: 2336184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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US-10-223-076-2
; Sequence 2, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223, 076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040, 315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339, 472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107, 771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103, 754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17

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5	1880	67.8	2090	15	US-10-223-076-10	Sequence 10, Appli
6	1854	66.9	1964	15	US-10-223-076-14	Sequence 14, Appli
7	1853.5	66.9	1621	13	US-10-425-114-10163	Sequence 10163, A
8	1849.5	66.7	1888	13	US-10-424-599-111496	Sequence 111496, A
9	1842.5	66.5	2099	15	US-10-223-076-12	Sequence 12, Appli
10	1833	66.1	1446	15	US-10-223-076-6	Sequence 6, Appli
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12	1279	46.2	1572	15	US-10-223-076-17	Sequence 17, Appli
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27	762.5	27.5	1497	15	US-10-278-733-3	Sequence 3, Appli
28	753.5	27.3	827	13	US-10-425-114-13703	Sequence 13703, A
29	753.5	27.3	1470	15	US-10-278-733-4	Sequence 4, Appli
30	751.5	27.1	1470	15	US-10-278-733-7	Sequence 7, Appli
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33	709.5	25.6	1895	14	US-10-157-855-14	Sequence 14, Appli
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no problem

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 FEATURE:
 NAME/KEY: CDS
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 US-10-223-076-2

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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-623-514A-2 (1-520) x US-10-223-C76-2 (1-1904)

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 QY 101 AlaAspAlaThrPheThrArgProSerValProAlaHisArgAlaArgGlySer 120
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 DB 499 CCACCTTAGCTCCGACGCAATCTTCAACAGAGCCATCGCGGATTTCAACCTCTGTGTA 558
 QY 141 ValValLeuLeuAlaValAsnSerArgLeuLeuLeuGluAsnLeuMetLysTyrGlyTyr 160
 DB 559 GTAGTCTTATTCGTGTAACAGTAGACTCATCATCGAAATCTTATGAAGATGTTGGTGG 618
 QY 161 LeuLeuArgThrAspPheThrPheSerArgSerLeuArgAspThrProLeuPheMet 180
 DB 619 TTGATCAGAACGATTTCTGTTTGTAGTTCAAGATCGCTGCGAGATTTGGCGGCTTTTCATG 678
 QY 181 CysCysLeuSerLeuSerLeuPheProLeuAlaAlaPheThrValGluLysLeuValLeu 200
 DB 679 TGTGTATATCCCTTCGATCTTCTCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 738
 QY 201 GlnLysTyrLeuSerGluProValLeuPheLeuHisLeuLeuLeuLeuLeuLeuLeu 220
 DB 739 CAGAAATACATATCAGAACTGTTGTCATCTTCTTCAATATATATCACCATGACAGAG 798
 QY 221 ValLeuTyrProValTyrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThr 240
 DB 799 GTTTTGTATCCAGTTTACGTCACCTTAAGGTGTCATCTCTCTTTCATCAGGTGTCACT 858
 QY 241 LeuMetLeuLeuThrCysLeuValThrLeuLysLeuValSerTyrAlaHisThrSerTyr 260
 DB 859 TTGATGCTCCTCACTTGCATTTGTGCTAAAGTTGGTTTCTTATGCTCATCTAGCTAT 918
 QY 261 AspLeuArgSerLeuAlaAspAlaAlaAspLysAlaAsnProGluValSerTyrTyrVal 280

DB 919 GACATAGATCCCTAGCAATGAGCTGATAGGCAATCCTGAGTCTCTCTACTAGCTT 978
 QY 281 SerLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyr 300
 DB 979 AGCTTGAAGAGCTTGGCATAATTTTCATGTCCTCCACATATTTGTATATCAAGGTTAT 1038
 QY 301 ProArgSerAlaCysLeuArgGlyTyrValAlaArgGlnPheAlaLysLeuValLeu 320
 DB 1039 CCACGTTCTGCATGATATACGAGAGGTTGGTGGCTCGCTCAATTTGCAAACTGGTCTAT 1098
 QY 321 PheThrGlyPheMetGlyPheLeuLeuGluGlnTyrLeuAsnProLeuValArgAsnSer 340
 DB 1099 TTCACCGGATTCATGGGATTTATAAGAACATATATAAATCCTATTGTGAGAACTCA 1158
 QY 341 LysHisProLeuLysGlyAspLeuLeuTyrAlaLeuGluArgValLeuLysLeuSerVal 360
 DB 1159 AAGCATCCTTTGAAAGGCGATCTTCTATATGCTATTGAAGAGTGTGGAAGCTTCAGTT 1218
 QY 361 ProAsnLeuTyrValTrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnLeu 380
 DB 1219 CCAATTTATATGTTGGCTCTGCAATTTCTACTGCTTCTCCACCTTGTGTTAAACATA 1278
 QY 381 LeuAlaGluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTyrTrpAsnAlaLys 400
 DB 1279 TTGGCAGAGCTTCTCTGCTTCGGGGATCGTGAATTTCTACAAAGATTGGTGGATGCAAAA 1338
 QY 401 SerValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHis 420
 DB 1339 AGTGTGGGAGTTACTGGGAATTTGGATATATCCCTGTTTCATTAATGGATGGTTCGACAT 1398
 QY 421 IleTyrPheProCysLeuArgSerLysIleProLysThrLeuAlaLeuLeuLeuAlaPhe 440
 DB 1399 ATATATTTCCGTCGCTTGCAGCAAGATACCAAGACACTCGCCATATATCATTTGCTTTC 1458
 QY 441 LeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeu 460
 DB 1459 CTAGTCTCTGAGCTTTTCATGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1518
 QY 461 TrpAlaPheLeuGlyLeuMetPheGlnValProLeuValPheLeuThrAsnTyrLeuGln 480
 DB 1519 TGGGCTTTTCTTGGGATTTATGTTTTCAGGTGCTTTCAGTTCATCAAACTATCTACAG 1578
 QY 481 GluArgPheGlySerThrValGlyAsnMetIlePheThrPheIlePheCysIlePheGly 500
 DB 1579 GAAAGGTTTGGCTTCACCGTGGGAGACATGATCTTCTGTTTCATCTTCTGATTTTCGA 1638
 QY 501 GlnProMetCysValLeuLeuTyrTyrHisAspLeuMetAsnArgLysGlySerMetSer 520
 DB 1639 CAACCGATGTTGCTTCTTCTTATACCAAGCTGATGAACCGAAAGGATCGATGTCAT 1698

RESULT 2

US-10-157-855-1
 Sequence 1, Application US/10157855
 Publication No. US20020170091A1
 GENERAL INFORMATION:
 APPLICANT: Laseuer, Michael W.
 APPLICANT: Ruzinsky, Diane M.
 TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
 TITLE OF INVENTION: Acid Sequences
 FILE REFERENCES: 1,651,158
 CURRENT APPLICATION NUMBER: US/10/157,855
 PRIOR FILING DATE: 2002-05-31
 PRIOR APPLICATION NUMBER: 09/326,203
 PRIOR FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 60/088,143
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/108,389
 PRIOR FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1942

Same, 9/5
Patent 6,440,476

Db 1077 AGC

Db 1077 AGCTTGAAGAGCTTGGCATATTTCATGGTCGCTCCACATTGTGTATCAGCCAAAGTTAT 113

ORGANISM: *Brassica napus*

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FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(11:07)
US-10-223-076-4

Alignment Scores:
Pred. No.: 7.5e-257      Length: 1537
Score: 2351.50          Matches: 447
Percent Similarity: 89.23%      Conservative: 17
Best Local Similarity: 85.96%      Mismatches: 37
Query Match: 84.86%      Indels: 19
DB: 15      Gaps: 5

US-09-623-514A-2 (1-520) X US-10-223-076-4 (1-1537)

QY 1 MetAlaileuAspSerAlaGlyValThrValThrGluAsnGlyGlyGluPhe 20
DB 22 ATGGAGATTTCGGATTCTGGAGCGGTCACTATCCGACGGAGAACGGTGGT----- 72
QY 21 ValAspLeuAspArgLeuArgArgLysSerArgSerAspSerSerAsnGlyLeuLeu 40
DB 73 GCGGATCTCGATACGCTCGTCCCGGAAACCGAGATCGGATCTTCCAAATGGACTTCCT 132
QY 41 LeuSerGlySerAspAsnSerProSerAspValGlyAlaProAlaAspValArg 60
DB 133 -----CCTGATCCCGTAACGTGTTCCGAT-----GCTGACGTGAGG 168
QY 61 AspArgileAspSerValValAsnAspAspAlaGlnGlyThrAlaAsnLeuAlaGlyAsp 80
DB 169 GATCGGGTTCGATTCAGCTGTT---GAGGATCTCAAGGAAAGCCAAATTTGGCGCGAGAA 225
QY 81 AsnAsnGlyGlyGlyAspAsnAsnGlyGlyGlyArgGlyGlyGluGlyArgGlyAsn 100
DB 226 AAGCAA-----ATTAGGAATCCGGTGGAGAACGGCGGGGGAAC 264
QY 101 AlaAspAlaThrPheThrTyrArgProSerValProAlaHisArgArgAlaArgGluSer 120
DB 265 GTGGATGTAAAGTACACATATCGCGCGTTCGGTTCAGCTCATCGGAGGTGGCGGAGAGT 324
QY 121 ProLeuSerSerAspAlaIlePheLysGlnSerHisAlaGlyLeuPheAsnLeuCysVal 140
DB 325 CCACCTCAGCTCTGACGCGCATCTTCAACACAGAGCCATGCTGGACATATTCAACCTGTGTGTA 384
QY 141 ValValLeuIleAlaValAsnSerArgLeuIleIleGluAsnLeuMetLysTyrGlyTyr 160
DB 385 GTAGTCTTGTTGCTGTAAACAGTAGACTCATCTATCGAAATCTCATGAAGTAGGTGG 444
QY 161 LeuIleArgThrAspPheThrPheSerSerArgSerLeuArgAspTrpProLeuPheMet 180
DB 445 TTGATCAGAACTGATTCTCGTTTGTAGTTCAACGCTCTCGGAGATTGGCCCCCTTTTCATG 504
QY 181 CysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGluLysLeuValLeu 200
DB 505 TGTGTGCTCTCCCTTCAATCTTTCCTTTGGCTGCCCTTACCGTCGAGAAATAGTACTT 564
QY 201 GlnLysTyrIleSerGluProValValIlePheLeuHisIleIleThrMetThrGlu 220
DB 565 CAGAAATGCATATCTGAACCTGTGTGATCATCTTCTCATATATATATATATATATATATAT 624
QY 221 ValLeuTyrProValTyrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThr 240
DB 625 GTCTGTATCCAGCTACGTCACCTCTAAGGTGTGATTCCGCCCTCTTATCAGGTGTCAAG 684
QY 241 LeuMetLeuLeuThrCysIleValThrLeuLysLeuValSerTyrAlaHisThrSerTyr 260
DB 685 TTGATGCTCCTCACTTGCATTTGTGTGCTGAAGTTGTTTCTTACGCTCATATACTAAT 744
QY 261 AspIleArgSerLeuAlaAsnAlaAlaAspLysAlaAsnProGluValSerTyrVal 280
DB 745 GACATAGAACCCCTAGCTAATCATCTGATAGGCCAATCTGGAAGTCTCTTACTATGTT 804
QY 281 SerLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyr 300

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DB 805 AGCTTCAGAGAGCTTGGCGTATTTTCATGCTTGCCTCCACATTTGTGTTATCAGCGAGCTAT 864
QY 301 ProArgSerAlaCysIleArgLysGlyTyrValAlaArgGlnPheAlaLysLeuValIle 320
DB 865 CCACGTTCTCCATGATATCCGAAAGGGTGGTGGCTCGTCAATTTGCAAGAGCTGATCATA 924
QY 321 PheThrGlyPheMetGlyPheIleIleGluGlnTyrIleAsnProIleValArgAsnSer 340
DB 925 TTCCTGGATTTCATGGATTATATAGACATATATATAATCTTATTTAGGAAGTCA 984
QY 341 LysHisProLeuLysGlyAspLeuLeuTyrAlaIleGluArgValLeuLysLeuSerVal 360
DB 985 AAACATCCTTTGAAAGGGGATCTCTATACGGTGTGAAAGAGTGTGAAAGCTTTCAGTT 1044
QY 361 ProAsnLeuTyrValTyrProLysCysMetPheTyrCysPhePheHisLeuTyrLeuAsnIle 380
DB 1045 CCAAAATTTATACGTGGCTCTCGATGTTCTATCTGCTTCTTCCACCTTTGGTTAAACATA 1104
QY 381 LeuAlaGluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAlaLys 400
DB 1105 TTGGCAGAGCTCTCTGCTTCGGGGATCGTGAATTTCTACAAAGATTGGTGGATGCAAAA 1164
QY 401 SerValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHis 420
DB 1165 AGCGTCGGAGATTATTGGAGATATGATATGCTGTTTCATATAATGGATGGTTCGACAT 1224
QY 421 IleTyrPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAlaPhe 440
DB 1225 GTATACCTTCGCGCTTCGAGAAATATACCGAAATACCGCTATATATCTTCTGCTTTC 1284
QY 441 LeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeu 460
DB 1285 TTAGTCTCTCAGCTCTTTCATGAGTTATGATCATGCGAGTCTCTTCTGCTCTCTCAAACTA 1344
QY 461 TrpAlaPheLeuGlyIleMetPheGlnValProLeuValPheIleThrAsnTyrLeuGln 480
DB 1345 TGCGCTTCTTGGGGGATTTATGTTTCAGGTGCTTGGTATTTATATACAAACTACTACAA 1404
QY 481 GluArgPheGlySerThrValGlyAsnMetIlePheThrPheIlePheCysIlePheGly 500
DB 1405 GAAAGGTTTGGCTCCATCGTGGGAAACATGATATCTGGTTTACCTTCTGCAATTTTCGA 1464
QY 501 GlnProMetCysValLeuLeuTyrTyrHisAspLeuMetAsnArgLysGlySerMetSer 520
DB 1465 CAACCGATGTGTGCTTCTTTATATACAGACTTGATGAACCGCAAGGAAGATGTCA 1524

RESULT 4
US-10-223-076-8
Sequence 8, Application US10223076
Publication No. US20030074695A1
GENERAL INFORMATION:
APPLICANT: Farese, Robert V
APPLICANT: Cases, Sylvaine
TITLE OF INVENTION: Plant Diacylglycerol C-transferase and
FILE REFERENCE: US10223076
CURRENT APPLICATION NUMBER: US/10/223,076
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 10/040,315
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1512
TYPE: DNA

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ORGANISM: Brassica napus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1512)
US-10-223-076-8

Alignment Scores:
Pred. No.: 4,48-252 Length: 1512
Score: 2303.50 Matches: 442
Percent Similarity: 88.10% Conservative: 17
Best Local Similarity: 84.84% Mismatches: 43
Query Match: 83.35% Indels: 19
DB: 15 Gaps: 5

US-09-623-514A-2 (1-520) x US-10-223-076-8 (1-1512)

Qy 1 MetAlaIeLeuAspSerAlaGlyValThrThr---ValThrGluAsnGlyGlyGlu 19
Db 1 ATGGCGATTGTTGGATTCTGGAGGGTGTCTGTACCGCGGACGGAGAACGGC-----51
Qy 20 PheValAspLeuAspArgLeuArgArgArgSerArgSerArgSerSerAsnGlyLeu 39
Db 52 GTCGGGATCTCGACAGGCTCCACCGTCGTAATCGAGTTCGGATTCTTCAACCGGACTC 111
Qy 40 LeuLeuSerGlySerAspAsnAsnSerProSerAspValGlyValAlaProAlaAspVal 59
Db 112 CTC-----TCGATACCTCCCGCTCGAGCGAGTGTGGAGCTTCGGCGCGCGAA 159
Qy 60 ArgAspArgLeuAspSerValValAsnAspAlaGlnGlyThrAlaAsnLeuAlaGly 79
Db 160 AGGATCGGGTGTATTCGCTCGCGAGGAGGAGGCTCAGGAAACAGCGAATTTAGCT---216
Qy 80 AspAsnAsnGlyGlyGlyAspAsnAsnGlyGlyArgGlyGlyGlyGluGlyArgGly 99
Db 217 -----GGCGGAGATGCCGAACACTAGGGAATCCGCGGAGGC-----252
Qy 100 AsnAlaAspAlaThrPheThrThrArgProSerValProAlaHisArgArgAlaArgGlu 119
Db 253 -----GATGTAAAGTTTACGTATACCGCTCGGTTCACSTCATCCGAGGAGGAGGAG 306
Qy 120 SerProLeuSerSerAspAlaIlePheGlyGlnSerHisAlaGlyLeuPheAsnLeuCys 139
Db 307 AGTCCTCTCAGTCGAGCTATCTTCAACAAAGCCATGCAGGATGTTTCAACCTCTGT 366
Qy 140 ValValValLeuLeuAlaValAsnSerArgLeuIleIleGluAsnLeuMetGlyThrGly 159
Db 367 GTAGTTGTCTTGTTCCTGTTTAAACAGTACATCATTCGAAACCTCATGAAGTATGCT 426
Qy 160 TrpLeuLeuArgThrAspPheThrPheSerArgSerLeuArgAspTrpProLeuPhe 179
Db 427 TGGTTGATCAGACACTGATTTTGGTTTGTATCTACATCTTACGAGACTGGCGGCTTTTC 486
Qy 180 MetCysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGluGlyValVal 199
Db 487 ATGTGTTGCTTCACTTCTGCTCTTCTTGGCTGCTTCACTTCACTTCACTTCACTTCA 546
Qy 200 LeuGlnGlyThrIleSerGluProValValIlePheLeuHisIleIleThrMetThr 219
Db 547 CTCAGAACTCATATCTGAGCGTGTGCTTTCATCTTCTGATTAATTAATTAATTAATTA 606
Qy 220 GluValLeuTrpProValTrpValThrLeuArgCysAspSerAlaPheLeuSerGlyVal 239
Db 607 GAGGCTTGTATCCAGTCTACGTACACTGAGGTGTGATCTGCTCTTGTTCAGGTGTC 666
Qy 240 ThrLeuMetLeuLeuThrCysIleValTrpLeuLeuValSerTrpAlaHisThrSer 259
Db 667 ACCTGTATGCTGCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Qy 260 TyrAspIleArgSerLeuAlaAsnAlaAlaAspGlyAlaAsnProGluValSerTrpThr 279
Db 727 TACGACATAAGAACCTCGCCAAATTCAGCTGATAGGTCGATCTGAAATCTCTACTAT 786
Qy 280 ValSerLeuLysSerLeuAlaThrPheMetValAlaProThrLeuLeuCysThrProSer 299

Db 787 GTTAGCTTGAAGAGCTTGGCGTATTTCATGGTGTCTCCACACTGTGTATCAGCAAGC 846
Qy 300 TyrProArgSerAlaCysIleArgLysGlyTrpValAlaArgGlnPheAlaLysLeuVal 319
Db 847 TATCCACGTTTCCATGTATCCGAAAGGTTGGTGGCTCGTCAACTTGCACAAACTGTC 906
Qy 320 IlePheThrGlyPheMetGlyPheIleIleGluGlnTrpIleAsnProIleValArgAsn 339
Db 907 ATATTCACTGAGCTCATGGGATTTATAATAGAGCAATATATAATCTTATTGTAGGAC 966
Qy 340 SerLysHisProLeuLysGlyAspLeuLeuTrpAlaIleGluArgValLeuLysLeuSer 359
Db 967 TCAAGACATCTCTGAAGGGGACCTCTATATGCTATTGAAGAGTGTGAAGCTTTCA 1026
Qy 360 ValProAsnLeuTrpValTrpLeuCysMetPheTrpCysPhePheHisLeuTrpLeuAsn 379
Db 1027 GTTCCAAATCTATATGTGTGGCTCTGCATGTTCTACTGCTTCTTCCACCTTTGGTTAAAC 1086
Qy 380 IleLeuAlaGluLeuLeuCysPheGlyAspArgGluPheTrpLysAspTrpTrpAsnAla 399
Db 1087 ATATTGGCAGAGCTCTCTGCTTCGGGACCGGTGAATTTTACAAAGATTGGTGAATGCA 1146
Qy 400 LysSerValGlyAspTrpArgMetTrpAsnMetProValHisLysTrpMetValArg 419
Db 1147 AAAACGCTGGAGATTATTGGAGATGTGAATATGCTGTTTCAAAATGGATGGTTCGA 1206
Qy 420 HisLeuTrpPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAla 439
Db 1207 CATGTATATCTTTCCGTGCTGCGCATCAAGATACCAAAAGTACCCGCCATTATCATGCT 1266
Qy 440 PheLeuValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLys 459
Db 1267 TTTTATGCTCTGAGTCTTTTATGAGTTATGATCGAGTTCCTTGGCGTCTCTTCAAT 1326
Qy 460 LeuTrpAlaPheLeuGlyIleMetPheGlnValProLeuValPheIleThrAsnTrpLeu 479
Db 1327 CTATGGGCTTTTCATGGGAATTATGTTTTCAGGTCCTTTTGGTCTTTATCAAACTTTTA 1386
Qy 480 GlnGluArgPheGlySerThrValGlyAsnMetIlePheThrPheIlePheCysIlePhe 499
Db 1387 CAAGAAAGGTTTGGCTCCATGTTGGGAAACATGATCTTTGGTTCAGCTTCTTGCATTTTC 1446
Qy 500 GlyGlnProMetCysValLeuLeuTrpTrpHisAspLeuMetAsnArgLysGlySerMet 519
Db 1447 GACAAACCGATGTGGGCTTCTTTTATACATGATGATGAAACCGAAAGGATTCATG 1506
Qy 520 Ser 520
Db 1507 TCC 1509
RESULT 5
US-10-223-076-10
Sequence 10, Application US/10223076
Publication NO. US20030074695A1
GENERAL INFORMATION:
APPLICANT: Eares, Robert V
APPLICANT: Cases, Sylvaine
TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
FILE OF INVENTION: Uses Thereof
FILE REFERENCE: UCAL-105CIP3
CURRENT APPLICATION NUMBER: US/10/223,076
CURRENT FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 10/040,315
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR FILING DATE: 1998-06-24

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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 1C
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Tropaeolum majus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(1727)
US-10-223-076-1C

Alignment Scores:
Pred. No.: 5,77e-203 Length: 2090
Score: 1880.00 Matches: 370
Percent Similarity: 78.11% Conservative: 44
Best Local Similarity: 69.81% Mismatches: 88
Query Match: 67.85% Indels: 28
DB: 5 Gaps: 10

US-09-623-514A-2 (-520): x US-10-223-076-10 (1-2090)

QY 1 MetAlaIleuAspSerAlaGlyValThrValThrGluAsnGlyGlyGluPhe 20
DB 171 ATGGCGGTGCAGAGTCGTCCACAGAACACAGACA---ACCATGAGTGTCCAGCGCAC--- 224
QY 21 ValAspLeuArgLeuArgAlaGlySerArgSerAsp-----SerSer 36
DB 225 TCGGATCTCAACAAATTCGCTAGAGAAACCGAGTTCCTCCGTGATTGAACCTTCGTGC 284
QY 37 AsnGlyLeuLeuSerGlySerAspAsnAsnSerProSerAspValGlyAlaPro 56
DB 285 TCCGGTTTACA-----TCCACCAATGGCGTACCGCG-----ACTGGCCACGTG 329
QY 57 AlaAspValArgAspArgIleAspSerValValAsnAspAspAlaGlnGlyThrAlaAsn 76
DB 330 GCTGAGAAATCGTGACCAAGATCCGGTAGGGCTATGGAGAACCAACAGGATCGGTCAAC 389
QY 77 LeuAlaGlyAspAsnAsnGlyGlyGlyAspAsnAsnGlyGlyGlyGlyGlyGlu 96
DB 390 TTAATTTGGA-----AATGTTGGAGCGTGTTCGCGGAATGAA 428
QY 97 GlyArg-----GlyAsnAlaAspAlaThrPheThrTyArgProSerValProAlaHis 114
DB 429 GAGAAACAGTAGGGGAGAGTATATACGATTACCTTACCGGCTTCGTTCCGGCTCAT 488
QY 115 ArgArgAlaArgGluSerProLeuSerSerAspAlaIlePheLysGlnSerHisAlaGly 134
DB 489 CCGAGGGTGGGAGAGTCTCTTAGCTCTGATGCAATCTTCAACAGAGCCCATGCGGGT 548
QY 135 LeuPheAsnLeuCysValValValLeuIleAlaValAsnSerArgLeuIleIleGluAsn 154
DB 549 TTATTCACACTGTGTATAGTGTGCTCAITTCAGTAAACAGTAGAGCTTATCATCGAAAT 608
QY 155 LeuMetLysTyArgGlyTrpLeuIleArgThrAspPheTrpPheSerSerArgSerLeuArg 174
DB 609 CTTATGAGATATGGTTGGTTGATCGATCTAGTCTGTTCTGTTTAACTCAAGATCACTGGGT 668
QY 175 AspTrpProLeuPheMetCysCysIleSerLeuSerIlePheProLeuAlaIlePheThr 194
DB 669 GATGTGTCATCTTATGCTGTCTATACACTCCCAATTTCCCACTGCTGCTGCTTTAT 728
QY 195 ValGluLysLeuValLeuGlnLysTrpIleSerGluProValValIlePheLeuHisIle 214
DB 729 GTTGAAAGCTGGTCAGCGAATATATATCTGAACTTGTGCTGTCTCTCTTCATGTA 788
QY 215 IleIleThrMetThrGluValLeuTyProValTyValThrLeuArgCysAspSerAla 234
DB 789 ATCGTTTCCACCGCTCCAGTTTATATCCAGTTATTGTGATCTTAACGTTGATTCGGTG 848
QY 235 PheLeuSerGlyValThrLeuMetLeuLeuThrCysIleValTrpLeuLysLeuValSer 254
DB 849 TATATGCTGGTGGTGTATGATGCTCTTGTGTTGCATATATGTTGAGCTGGTGTCA 908

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QY 255 TyAlaHisThrSerTyArgSerLeuAlaAsnAlaAlaAspLys-----Ala 272
DB 909 TATGGCATACACTAGTTCTGTATATAGAACACTGGCCAAATCTGCTATAGGGGATCGG 968
QY 273 AsnPro-----GluValSerTyTrpValSerLeuLysSerLeuAlaTy 287
DB 969 CACCCCAATTCACCACTTGTGAGTGTCTCATATGATGTAGCTTGAAGAGATTGGCATAC 1028
QY 288 PheMetValAlaProThrLeuCysTyArgProSerTyProArgSerAlaCysIleArg 307
DB 1029 TTCATGGTGGCGCGCATTTATGTTACCGCTAGCTATCTCTGCTGCTGTATCCGC 1088
QY 308 LysGlyTrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPhe 327
DB 1089 AAGGGTGGGTGTTGCTGCTCAATTTGCAAACTAATAGTTTTCATAGACTCATGGGTTTC 1148
QY 328 IleIleGluGlnTyTrpIleAsnProIleValArgAsnSerLysHisProLeuLysGlyAsp 347
DB 1149 ATTATAGAACATATATATATCTATCTGTTTCGAAATTCCAACACCCCATTTGAAGAGAT 1208
QY 348 LeuLeuTyAlaIleGluArgValLeuLysLeuSerValProLeuLeuTyValTrpLeu 367
DB 1209 TTTTATATGCAATAGAGAGAGTTTGAAGCTTTCAGTTCCAATCTATATGTTGCTT 1268
QY 368 CysMetPheTyCysPhePheHisLeuTrpLeuAsnIleLeuAlaGluLeuLysCysPhe 387
DB 1269 TGCATGTTCTACTCTTTTCCACCTCTGCTGAACATACTGGCTGAGCTTCTTCGCTTT 1328
QY 388 GlyAspArgGluPheTyLysAspTrpTrpAsnAlaLysSerValGlyAspTyTrpArg 407
DB 1329 GGTGATCGTGAATCTACAAAGATGTGTGAATTCGCAAAACTGTTCGGAGTATTGAAA 1388
QY 408 MetTrpAsnMetProValHisLysTrpMetValArgHisIleTyPheProCysLeuArg 427
DB 1389 ATGTGGATATGCTGTTCAATGATGATGTTGCTGCTATATATTTCTCTGTTGAGG 1448
QY 428 SerLysIleProLysThrLeuAlaIleIleAlaPheLeuValSerAlaValPheHis 447
DB 1449 AATGGCATACCCAAAGAGGTGCCATTATATCGGTTCTTAGTTCTGGTGTCTTCCAT 1508
QY 448 GluLeuCysIleAlaValProCysArgLeuPheLysLeuTrpAlaPheLeuGlyIleMet 467
DB 1509 GAGCTCTGCATTCAGTCTCTTCCAGTATTCAAGTATTGGGCTTATAGGCATTATG 1568
QY 468 PheGluValProLeuValPheIleThrAsnTyLeuGlnGluArgPhe---GlySerThr 486
DB 1569 TTTCAAGTTCCTTGGTGTATGATTCGAATATATACAGAAAGTTCAGTAAATCTATG 1628
QY 487 ValGlyAsnMetIlePheTrpPheIlePheCysIlePheGlyGlnProMetCysValLeu 506
DB 1629 GTGGCAATATGATCTTCTGTTCACTCTGCTGATACTTGGCCAACTATGTGTGCTT 1688
QY 507 LeuTyTrpHisAspLeuMetAspArgLys 516
DB 1689 CTATATACCATGACCTGATAAATCTAAAG 1718

RESULT 6
US-10-223-076-14
; Sequence 14, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; FILE REFERENCE: Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/223,076
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771

```



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; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Piralla frutescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1673)
US-10-223-076-14

Alignment Scores:
Pred. No.: 4,73e-200 Length: 1964
Score: 1854.00 Matches: 359
Percent Similarity: 74.18% Conservative: 49
Best Local Similarity: 65.27% Mismatches: 92
Query Match: 66.91% Indels: 50
DB: 15 Gaps: 9

US-09-623-514A-2 (1-520) x US-10-223-076-14 (1-1964)

Qy 1 MetLalleLeuAspSerAlaGlyValThrValThr-----GluAsnGly 16
Db 69 ATGGCGATCTTGGACTCGCGAGATCTGACACGAGCGTGTCCAGTGGCGGACAAACGCG 128
Qy 17 GlyGlyGluPheValAspLeuAspArgLeuArgArgLysSerArgSerAspSer 36
Db 129 GCGGCACATCACACACTCTT-----CGCCGGAGACAAAGTCGCGCTCCGCT 182
Qy 37 AsnGlyLeuLeuSerGlySerAspAsnAsnSerProSerAspValGlyAlaPro 56
Db 183 -----CTTCTCGACTCGGATTCACACTCTCTG----- 209
Qy 57 AlaAspValArgAspArgIleAspSerValValAsnAsp-----AspAlaGlnGlyThr 74
Db 210 -----GAGGCGAGAGAGCGCAATCAATGATTCGAAATGTTTCGAAACGAC 254
Qy 75 AlaAsnLeuAlaGlyAspAsnAspGlyGly----- 84
Db 255 GCTAATTGTATCGAAATCTCCGCGGAGCCGCTGGATCCGAGAACGAAHAACAGAG 314
Qy 85 -----GlyAspAsnAsnGly-----GlyGlyArgGlyGlyGly 96
Db 315 AGTTATGTTAAGGAGGAGGCGGCGAAAGTGAAGAGAAATGAGAAACTAGTAATGGCAAC 374
Qy 97 GlyArgGlyAsnAlaAspAlaThrPheThrTyrArgProSerValProAlaHisArgArg 116
Db 375 GGAACGTGATGTATGGCGGTCAAAATTCACATTCAGCGCGCGCGCTGTCTCACCGCAA 434
Qy 117 AlaArgGluSerProLeuSerSerAlaIlePheLysGlnSerHisAlaGlyLeuPhe 136
Db 435 AATAAGAGAGTCTCTTAGCTCCGAGCCCATCTTCAACAGAGCCATGAGGCTCTTC 494
Qy 137 AsnLeuCysValValValLeuAlaValAsnSerArgLeuIleGluAsnLeuMet 156
Db 495 AACCTTTGTATAGTGGTCTTGTGCTGTAATAGCAGACTAATAATTTGAAATTTAATG 554
Qy 157 LysTyrGlyTrpLeuIleArgThrAspPheThrPheSerSerArgSerLeuArgAspTrp 176
Db 555 AAGTATGGGTGCGTGAATCAATAGGATTTTGGTTTAGTTCAACATCGCTTAGGATGG 614
Qy 177 ProLeuPheMetCysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGlu 196
Db 615 CCATGCTATATGTGTGTGTAGTCTTCCAGTTTTCGAC:CGCTTCATTTCTTGTGCGAG 674
Qy 197 LysLeuValLeuGlnLysTyrIleSerGluProValIlePheLeuHisIleIle 216
Db 675 AAGTTGGTGAACATAAATTATATACCTGAGTGGGTCCGAGCTTCTTTCATGTTACAACT 734

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Qy 217 ThrMetThrGluValLeuTyrProValTyrValThrLeuAtqCysAspSerAlaPheLeu 236
Db 735 ACAACAGTSGAAATCTTGTTCACAGTTGTGTTCATCTTAGGTGATGATCTCTGCTCTA 794
Qy 237 SerGlyValThrLeuMetLeuLeuThrCysIleValTrpLeuLysLeuValSerValAla 256
Db 795 TCAGGTGTACGCTAATGCTCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 854
Qy 257 HisThrSerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLys----- 271
Db 855 CATACAAACTATGATTTGAGAGTACTTCGCAAAATCATTGATAAGTGGAGAGCTATGCTC 914
Qy 272 -----AlaAsnProGluValSerTyrValSerLeuLysSerLeuAlaTyrPheMet 289
Db 915 AGGTACTGGAAACCTCGACTACGCTTATGATGTAAGCTTTAAGAGTCTGGCATACTTCA 974
Qy 290 ValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAlaCysIleArgLysGly 309
Db 975 GTTGTCTCTCATATTGTGTACAGCAAGCTACCTCGACAGCTTGCATTCGGAAGGT 1034
Qy 310 TrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIleIle 329
Db 1035 TCGGTGTGTAGGCAACTAATTAAGCTGCTAATATTACAGGACTCATGGGATTTATTATA 1094
Qy 330 GluGlnTyrIleAsnProIleValArgAsnSerLysHisProLeuLysGlyAspLeuLeu 349
Db 1095 GAACAGTACATAAAACCCGATGCTTCAAAATCTCAACATCTCTGAAAGAAACCTTTTA 1154
Qy 350 TyrAlaIleGluArgValLeuLysLeuSerValProAsnLeuTyrValTrpLeuCysMet 369
Db 1155 TATGCCATTGAGAGGTCTTGAAGCTTCTGTTCCAAAATTATATGTGTGGCTCTGCATG 1214
Qy 370 PheTyrCysPhePheHisLeuTrpLeuAsnIleLeuAlaGluLeuLeuCysPheGlyAsp 389
Db 1215 TTTTATGTTTTCACCTCTGGCTAATAATATATCTGTCTGAACITCTGTGCTTTGGGAC 1274
Qy 390 ArgGluPheTyrLysAspTrpTrpAsnAlaLysSerValGlyAspTyrTrpArgMetTrp 409
Db 1275 CGTGAATTTTATAAGGATTTGGTGGATTCGAGGACAGTGGAGGATCTCGGAATGTGG 1334
Qy 410 AsnMetProValHisLysTrpMetValArgHisIleTyrPheProCysLeuArgSerLys 429
Db 1335 AATATGCTGTTCATAAATGATGATGCTGCGCATATATATCTGCTTACAAAATGGA 1394
Qy 430 IleProLysThrLeuAlaIleIleAlaPheLeuValSerAlaValPheHisGluLeu 449
Db 1395 ATACCAAGATAGTGGCAGTTTGTATCGCTTCTTGTCTGCGATTTTTCATGAGCTG 1454
Qy 450 CysIleAlaValProCysArgLeuPheLysLeuTrpAlaPheLeuGlyIleMetPheGln 469
Db 1455 TCGTGTGAGTCCCTTTGCCAAATATTCAAGTTTGGGGGTCTCGGGTATCATGCTTCAG 1514
Qy 470 ValProLeuValPheIleThrAsnTyrLeuGlnGluArgPhe---GlySerThrValGly 488
Db 1515 GTTCTCTCGTAATCGTGACTAATTTACTTCAAGAAAGTTCAAAACTCAATGTGTGGC 1574
Qy 489 AsnMetIlePheTrpPheIlePheCysIlePheGlyGlnProMetCysValLeuLeuTyr 508
Db 1575 AATATGATGTTCTGCTGCTTCTTCTGATCTTGTGTCACCATCTGTGTGTGTCTGTAC 1634
Qy 509 TyrHisAspLeuMetAsnArgLysGlySer 518
Db 1635 TACCACGACTTGATGATCGAATCGAATGCTAGT 1664

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RESULT 7

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US-10-425-414-10163
; Sequence 10163, Application US/10425114
; Publication No. US:0040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

```

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; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10163
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 7C0896419_FLI
US-10-425-114-10163

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Alignment Scores:
Pred. No.: 3,92e-200 Length: 1621
Score: 1853.50 Matches: 359
Percent Similarity: 76.25% Conservative: 52
Best Local Similarity: 66.60% Mismatches: 85
Query Match: 66.89% Indels: 43
DB: 13 Gaps: 9

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US-09-623-514A-2 (1-520) x US-10-425-114-10163 (1-1621)

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QY 1 MetAlaIleLeuAsp-----SerAlaGlyValThrThrValThrGluAsnGlyGly 17
DB 65 ATGGGATCTCCGATGCGCTGCGCGCTGGCAGCGCCACTACCCAGC-----118
QY 18 GlyGluPheValAspLeuAspArgLeuArgArgArgLysSerArgSerSerAsn 37
DB 119 -----CACTCAGAT-----CTCGACAGCCCTCTCTGCGCGCAGGTCTCCGCC 163
QY 38 GlyLeuLeuLeu-----SerGlySerAspAsnAsnSerProSerAspAsp 52
DB 164 GAGTCTCTCTGACGCTGCCAGATTCGGCTCCGACATTC-----208
QY 53 ValGlyAlaProAlaAspValArgAspArgIleAspSerValValAsnAspAlaGln 72
DB 209 -----CTGACCGGCAAAATCACCGACGAC---GAC 235
QY 73 GlyThrAlaAsnLeuAlaGlyAspAsnAsnGlyGlyGlyAspAsnGlyGlyArg 92
DB 236 AACATCAAGATCACAGCCGATATATACGACGCTCCGACGACAAATGGCGCGGCC 295
QY 93 GlyGlyGlyGlyGlyArgGlyAsn-----AlaAspAlaThrPheThrArg 108
DB 296 GCCAATGACCTGGCAGGAGCCGACACCGCTGCGCGATTCAAATAGCTTACCGT 355
QY 109 ProSerValProAlaHisArgAlaArgGluSerProLeuSerSerAspAlaIlePhe 128
DB 356 CCCTCCGCTCCCGCAGCCGACAGATCAAGAGAGCCCTTAGCTCCGACACATCTTC 415
QY 129 LysGlnSerHisAlaGlyLeuPheAsnLeuCysValValValLeuIleAlaValAsnSer 148
DB 416 AGACAGAGTATCAGGAGCTGTCAATCTCTGCATAGTAGTGTGTGTGTCGCGGACAGC 475
QY 149 ArgLeuIleIleGluAsnLeuMetLysTyrGlyTrpLeuIleArgThrAspPheTrpPhe 168
DB 476 AGACTTATCATGAGANTTTAATGAGTAGTGTGTGTGATCAAGTAGCTTTGGTTT 535
QY 169 SerSerArgSerLeuArgAspTrpProLeuPheMetCysCysLeuSerLeuSerIlePhe 188
DB 536 AGTTCAAAATCAITGAGAGATGGCCCTCTCTCATGTGCTGTCTTAGCTTTGCCATATT 595
QY 189 ProLeuAlaIlePheThrValGluLysLeuValLeuGlnLysTyrIleSerGluProVal 208
DB 596 CCACTTGCTGCTTTGTGTGGAAAGGTGGCACAACAAAGGTGTA-TTCTGAACCAAGTT 655
QY 209 ValIlePheLeuHisIleIleIleThrMetThrGluValLeuTyrProValTyrValThr 228

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DB 556 GTTGTCTACTTCATCTAATAATATCAACTGTGTGAAGTGTCTATCCGGTTTAGTAATA 715
QY 229 LeuArgCysAspSerAlaPheLeuSerGlyValThrLeuMetLeuLeuThrCysIleVal 248
DB 716 CTCAGGTGTGATCTCTCTTTGTATCTGGTGTCACTGTGTATTAACCTTGCATTTGTG 775
QY 249 TrpLeuLysLeuValSerTyrAlaHisThrSerTyrAspIleArgSerLeuAlaAsnAla 268
DB 776 TGGTTTAAATTTGGTGTGCATATGCATACAACTATGATATGAGAGACCTTACTGTTTCG 835
QY 269 AlaAspLysAlaAsnPro-----GluValSerTyrValSer 281
DB 836 AATGAAAGGGGAAACATTTACCAATCTTGTATGAGTATCGTACACCTGTCACC 895
QY 282 LeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyrPro 301
DB 896 TTCAGGAGTTTGGCATCTTCATGGTGTCTTACATATGCTATCAGACAAAGCTATCCT 955
QY 302 ArgSerAlaCysIleArgLysGlyTrpValAlaArgGlnPheAlaLysLeuValIlePhe 321
DB 956 CGCACACCTTCAGTTTCGAAAGGGTGTGGTGTTCGTCAACTGTGACAGCTGATTAATTT 1015
QY 322 ThrGlyPheMetGlyPheIleIleGluGlnTyrIleAsnProIleValAlaArgAsnSerLys 341
DB 1016 ACAGGAGTTATGGGATTTATATAGAACATATATGATCTATTTACAAACCTCACT 1075
QY 342 HisProLeuLysGlyAspLeuLeuTyrAlaIleGluArgValLeuLysLeuSerValPro 361
DB 1076 CATCTTTGAAGGAAACCTTCTATATGCCATTCGAGAGATTTCTGAAGCTTTCTGTCCCA 1135
QY 362 AsnLeuTyrValTrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnIleLeu 381
DB 1136 AATGTATGTGTGGCTCTCATGCTCTCTACTCTTTTCCACCTTTGGTTAAATATATCTT 1195
QY 382 AlaGluLeuLeuCysPheGlyAspArgGlyPheTyrLysAspTrpTrpAsnAlaLysSer 401
DB 1196 GCAGAGCTTCTCGATTTGGTGTGATCGTGAGTCTCTATAAGATTTGGTGAATGCCAAA 1255
QY 402 ValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHisIle 421
DB 1256 GTTGAGAGTATGCGAGGATGGAATATGCTGTGCACAAATGATGGTTCGCCACATA 1315
QY 422 TyrPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleAlaPheLeu 441
DB 1316 TATTTTCCATGCTTAAGCGGTATACCCAGGGTGTCTGCTCAATTAATTCATTTCTG 1375
QY 442 ValSerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeuTrp 461
DB 1376 GTTCTGCTGTGTTTCATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1435
QY 462 AlaPheLeuGlyIleMetPheGlnValProLeuValPheIleThrAsnTyrLeuGlu 481
DB 1436 SCTTTATAGAAATATGTTTCAGGTTCTTGTGCTGTGATCACTAATAACCTCCAAAT 1495
QY 482 ArgPhe--GlySerThrValGlyAsnMetIlePheTrpPheIlePheCysIlePheGly 500
DB 1496 AAATACGAAACCTCAATGGTTGGAAATATGATTTTGGTTCATATTTGTATCTTGGT 1555
QY 501 GlnProMetCysValLeuLeuTyrTyrHisAspLeuMetAsnArgLysGlySerMet 519
DB 1556 CAACCAATGAGCTACTATTGTACTACCATGACTTGATGAATAGAAAGGAGAGATT 1612

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RESULT 8

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US-10-424-599-111496
; Sequence 111496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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Qy	249	T	r	p	L	e	u	s	L	e	u	V	a	l	S	e	r	T	y	r	A	l	a	H	i	s	T	h	r	S	e	r	T	y	r	A	s	p	l	e	A	r	g	S	e	r	L	e	u	A	s	n	A	l	a	268
Db	984	T	G	G	T	T	A	A	A	T	T	G	T	G	T	C	A	T	A	T	G	C	A	C	A	A	A	C	T	A	T	G	A	T	G	A	G	A	C	A	C	T	A	C	T	G	T	T	C	G	1043					
Qy	269	A	l	a	S	p	l	e	S	a	a	S	n	P	r	o	-----	G	l	u	V	a	l	S	e	r	T	y	r	V	a	l	S	e	r	281																				
Db	1044	A	A	T	G	A	A	A	G	G	A	A	A	C	N	T	T	A	C	C	A	T	A	C	T	T	G	A	T	T	G	A	G	A	T	T	C	G	A	C	T	G	A	C	T	G	A	C	1103							
Qy	282	L	e	u	S	e	r	L	e	u	A	l	a	T	y	r	P	h	e	M	e	t	V	a	l	a	P	r	o	T	h	L	e	u	C	y	s	T	y	r	G	l	n	P	r	o	S	e	r	T	y	r	P	r	o	301
Db	1104	T	T	C	A	G	G	A	G	T	T	T	G	C	A	T	T	C	A	T	T	C	A	T	T	A	T	G	C	T	A	T	T	G	C	A	T	A	T	G	C	A	T	A	T	G	C	A	G	A	C	T	A	C	T	1163
Qy	302	A	r	S	e	r	A	l	a	C	y	s	L	e	u	A	r	g	S	e	r	G	l	n	P	h	e	L	a	S	e	r	L	e	u	P	h	e	321																	
Db	1164	C	G	C	A	C	C	T	T	C	A	G	T	T	C	A	A	A	G	G	T	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1223							
Qy	322	T	h	r	G	l	y	P	h	e	M	e	t	G	l	y	P	h	e	L	e	l	L	e	G	l	u	G	l	n	T	y	r	L	e	A	s	n	P	r	o	L	e	u	A	s	n	S	e	r	L	y	s	341		
Db	1224	A	C	A	G	G	A	T	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	1283						
Qy	342	H	i	s	P	r	o	t	e	u	S	e	r	G	l	y	A	s	p	L	e	u	T	y	r	A	l	a	I	e	G	l	u	A	r	g	V	a	l	L	e	u	S	e	r	V	a	l	P	r	o	361				
Db	1284	C	A	T	C	T	G	A	A	G	G	A	A	C	T	C	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	1343						
Qy	362	A	s	n	L	e	u	T	y	r	P	r	o	L	e	u	C	y	s	M	e	t	P	h	e	T	y	r	C	y	s	P	h	e	H	i	s	L	e	u	T	r	P	L	e	u	A	s	n	L	e	u	381			
Db	1344	A	A	T	G	T	A	T	A	T	G	T	G	C	T	C	A	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1403								
Qy	382	A	l	a	G	l	u	L	e	u	C	y	s	P	h	e	G	i	y	A	s	p	L	e	u	G	l	u	P	h	e	T	y	r	L	y	s	A	s	p	T	r	P	r	o	A	s	n	A	l</						


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; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1107)
US-10-223-076-6

Alignment Scores:
Pred. No.: 6,99e-198 Length: 1446
Score: 1833.00 Matches: 342
Percent Similarity: 95.65% Conservative: 10
Best Local Similarity: 92.93% Mismatches: 16
Query Match: 66.15% Indels: 1
DB: 15 Gaps: 0

US-09-623-514A-2 (1-520) x US-10-223-076-6 (1-1446)
QY 153 GlnAsnLeuMetLysTyrGlyThrProLeuLeuArgThrAspPheTrpPheSerSerArgSer 172
DB 2 GAAATATCTCATGAAGTACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 61
QY 173 LeuArgAspTrpProLeuPheMetCysCysIleSerLeuSerIlePhePheProLeuAla 192
DB 62 CTGCAGATG-CGCGTTTTCATGCTGTCTCTCCCTTCAATCTTCTTCTTCTTCTTCTTCTTCT 120
QY 193 PheThrValGluLysLeuValLeuGlnLysTyrIleSerGluProValValIlePheLeu 212
DB 121 TTATCCGTCGAGAAATTAGTACTTCAGAAATGCATATCTGAACCTGTTGTCATCTTCTTCT 180
QY 213 HisIleIleThrMetThrGluValLeuTyrProValTyrValThrLeuArgCysAsp 232
DB 181 CATGTTATATACCATCACCAGGCTCTGTATCCAGCTATGTCTCTCTCTCTCTCTCTCTCTCT 240
QY 233 SerAlaPheLeuSerGlyValThrLeuMetLeuLeuThrCysIleValTrpLeuLysLeu 252
DB 241 TCTGCTTCTTATCAGGTGACAGCTGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 253 ValSerTyrAlaHisThrSerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLysAla 272
DB 301 GTTCTTACGCTCATACTAACTATCAGTATAGAACCTAGCTAGTAACTCATCTCTATAGGCC 360
QY 273 AsnProGluValSerTyrTyrValSerLysSerLeuAlaTyrPheMetValAlaPro 292
DB 361 AATCTCTGAAGTCTCTCTACTATG-TAGCTTGAAGAGCTTGGCTTTATTCATGCTTGTCTCC 420
QY 293 ThrLeuCysTyrGlnProSerTyrProArgSerAlaCysIleArgLysGlyTrpValAla 312
DB 421 ACATCTGTGTATCAGCAAGCTATCCAGTTCTCCATGTATCCGGAAGGGTGGTGGCT 480
QY 313 ArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIleIleGluGlnTyr 332
DB 481 CGTCAATTGCAAAACCTGCTATATTCATGCACTCATGGGATTTATATATAGCAATAT 540
QY 333 IleAsnProIleValArgAsnSerLysHisProLeuLysGlyAspLeuLeuTyrAlaIle 352
DB 541 ATAAATCTTATGTTAGGAACCTCAAGCATCTCTGAAAGGGGGAGCTTCTATATGCTATT 600
QY 353 GlnArgValLeuLysSerValProAsnLeuTyrValTrpLeuLysMetPheTyrCys 372

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DB 601 GAAAGAGTGTTCAGAGCTTTTCAGTTCCAATCTATATGTGTGGCTCTGCAATGTTCTACTGC 660
QY 373 PhePheHisLeuTrpLeuAsnIleLeuAlaGluLeuLeuCysPheGlyAspArgGluPhe 392
DB 661 TTCTTCCACCTTTGGTTAAACATATTGGCAGAGCTCTCTGCTTCGGGGACCGTGAATTC 720
QY 393 TyrLysAspTrpTyrAsnAlaLysSerValGlyAspTyrTrpArgMetTrpAsnMetPro 412
DB 721 TACAAAGATTGGTGGATGCAAAAACCGTTGGAGATTATGGAGATGTGGAAATATGCGCT 780
QY 413 ValHisLysTrpMetValArgHisIleTyrPheProCysLeuArgSerLysIleProLys 432
DB 781 GTTCACAAATGGATGGTTCGACATGTATATTTCGCTGCTGCGCATCAAGATACCAAAA 840
QY 433 ThrLeuAlaIleIleIleAlaPheLeuValSerAlaValPheHisGluLeuCysIleAla 452
DB 841 GTACCCGCCAATTATCATTTCTTTAGTCTCTGCGAGTCTTTTCATGAGTTTATCATCGCA 900
QY 453 ValProCysArgLeuPheLysLeuTyrAlaPheLeuGlyIleMetPheGlnValProLeu 472
DB 901 GTTCTTGGCGTCTCTTCAATCTATGGGCTTTTCATGGGAATTAATGTTTCAAGTCCCTTTG 960
QY 473 ValPheIleThrAsnTyrLeuGlnGluArgPheGlySerThrValGlyAsnMetIlePhe 492
DB 961 GTCTTTTATCAGAAACTTTTCAAGAAAGGTTTGGCTCCATGGTGGGAAACATGATCTTT 1020
QY 493 TrpPheIlePheCysIlePheGlyGlnProMetCysValLeuLeuTyrTyrHisAspLeu 512
DB 1021 GGTTCAGCTTCTTGCATTTTCGACAAACCGATGTGTGGGCTTCTTTATTACCATGACCTG 1080
QY 513 MetAsnArgLysGlySerMetSer 520
DB 1081 ATGACCCGCAAGGATCCATGTCC 1104

RESULT 11
US-10-260-238-310
; Sequence 310, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Rudworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FIDE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 310
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (6)..(6)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (10)..(10)

```

OTHER INFORMATION: n = any nucleotide
US-10-260-238-310

Alignment Scores:

Pred. No.: 3,65e-142 Length: 1150
Score: 1342.00 Matches: 272
Percent Similarity: 75.18% Conservative: 40
Best Local Similarity: 65.54% Mismatches: 56
Query Match: 48.43% Indels: 49
DB: 16 Gaps: 8

US-09-623-514A-2 (1-520) x US-10-260-238-310 (1-1150)

```

QY 112 ProAlaHisArgAlaArgGluSerProLeuSerSerSerSpAlaIlePheLysGlnSer 131
DB 4 CCGGCCNACCGCGCGCTGAGGAGAGCCCTCAGCTCCGACCCATCTTCGCCGACAGC 63
QY 132 HisAlaGlyLeuPheAsnLeuCysValValValLeuIleAlaValAsnSerArgLeuIle 151
DB 64 CATGCGAGCCTTCGAACCTATGCTATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
QY 152 IleGluAsnLeuMetLys-TyrGlyTrpLeuIleArgThrAspPheTrpPheSerAr 171
DB 124 ATTGAGAAATTAATGAAGGTATGCGCTACTACTAAATTAGAGCTGGATTTTGGTTAGTGAAC 183
QY 171 gSerLeuArgAspTrpProLeuPheMetCysCysIleSerLeuSerIlePheProLeuAl 191
DB 184 ATGCGTGGCAGATGGCCCTCTTCATGTGCTGCTC-ACCTTACCAACTTTCGCGCTGC 242
QY 191 aAlaPheThrValGluLysLeuValLeuGlnLysTyrIleSerGluProValValIlePh 211
DB 243 TGCACCTATGCTGAGAGAGTGGCTCAAGAAACCTATTATGATAA-----CA 290
QY 211 eLeuHisIleIleIleThrMetThrGluValLeuTyrProValTyrValThrLeu--Arg 230
DB 291 TCTCCATATCGTTATTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
QY 231 CysAspSerAlaPheLeuSerGlyValThrLeuMetLeuLeuThrCysIleValTrpLeu 250
DB 351 TGTGATCGCAGATATTATCTGATTTGTTGATGTTTCTTCAAGCACTATTATGTTGTTG 410
QY 251 LysLeuValSerTyrAlaHisThrSerTyrAspIleArgSerLeuAlaAsnAlaAsp 270
DB 411 AGCTTGTCTTTTCTCTCATACAATATGATATAGATATGCTGCTCCAAAGTATTGAA 470
QY 271 LysAlaAsnProGluValSerTyrTyrValSerLysSerLeuAlaTyrPheMetVal 290
DB 471 AAG-----TTTAAAGGCTATCTCTACTTCTCATGTTG 500
QY 291 AlaProThrLeuCysTyr--GlnProSerTyrProArgSerAlaCysIleArgLysGly 309
DB 501 GCCCAACACTTGTGTACCGAGCCGAGGTATCCCGAACTACATATATTAGAAAGGT 560
QY 310 TrpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMetGlyPheIleIle 329
DB 561 TGCGTGTGTCGCAACTGATAAAATGCTGTTTACAGGCTTGATGGGTTTATAATT 620
QY 330 Glu-----GlnTyrIleAsnProIleValArgAsnSerLysHisProLeuLys 345
DB 621 GAGCAATTTATTTTTCAGTACATAAAATCCAAATTTGTGAAGAATTCGAAGCATCCATTGAAA 680
QY 346 GlyAspLeuLeuTyrAlaIleGluArgValLeuLysLeuSerValProAscLeuTyrVal 365
DB 681 GGGAAATTTCTTGAATGCTATAGAGAGATATTGAATATTACGTGCCCAACATTATATGTC 740
QY 366 TrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnIleLeuAlaGluLeuLeu 385
DB 741 TGCGTTTGATGTTCTACTCGTTTTCCTCTCTG-TTGAATATTTCTTGAGCTCCCTC 799
QY 386 CysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAlaLysSerValGlyAspTyr 405
DB 800 TGTTTTGGTATCGTGAATTTCTAAGGACTGTTGGAATCCCAAAACAGTTGAAGAG-- 856

```

```

QY 406 TrpArgMetTrpAsnMetProValHisLysTyrTrpMetValArgHisIleTyrPheProCys 425
DB 857 -----CCTGTTCAAGAGTGGTCAATTCGACATATATATTTTCCATGTC 896
QY 426 LeuArgSerLysIleProLysThrLeuAlaIleIleAlaPheLeuValSerAlaVal 445
DB 899 ATAAGGAATGGT----- 910
QY 446 PheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeuTrpAlaPheLeuGly 465
DB 911 TTTTCAAGCTATGTTGCTGCTTCCATGCCACATTTTAAATTTCTGGGCATTTATTGGG 970
QY 466 IleMetPhe---GlnValProLeuValPheIleThrAsnTyrLeuGlnGluArgPheGly 484
DB 971 ATCATGTTTTCAGCAGATTTCCCTGGTATTCTTGACGAATACCTTCAGATATAATTCAAT 1030
QY 485 SerThr---ValGlyAsnMetIlePheTrpPheIlePheCysIlePheGlyGlnProMet 503
DB 1031 AACACAATGTTGGGCAACATGATATTTTGTCTCTTCAGCATCTCTGGGCAACCAATG 1090
QY 504 CysValLeuLeuTyrTyrHisAspLeuMetAsnArgLys 516
DB 1091 TGTGTTCTCTTATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129

```

RESULT 12

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US-10-223-076-17
; Sequence 17, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; TITLE OF INVENTION: Plant diacylglycerol O-transferase and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Zea mays
US-10-223-076-17

```

Alignment Scores:

Pred. No.: 9.08e-135 Length: 1572
Score: 1279.00 Matches: 232
Percent Similarity: 65.50% Conservative: 49
Best Local Similarity: 54.08% Mismatches: 69
Query Match: 46.16% Indels: 79
DB: 15 Gaps: 3

US-09-623-514A-2 (1-520) x US-10-223-076-17 (1-1572)

```

QY 166 PheTrpPheSerSerArgSerLeuArgAspTrpProLeuPheMetCysCysIleSerLeu 185
DB 1 TTTTGGTTTAAATGCTATCATTCATTCGAGAGCTGGCACTGCTAATGTTGCTTAGTCTA 60
QY 186 SerIlePheProLeuAlaIlePheThrValGluLysLeuValLeuGlnLysTyrIleSer 205
DB 61 CCATATTTTCCCTTGTGCTATTCGATGCTGAAAGTTGGCATTCACATCTCTGTTAGT 120
QY 206 GluProValValIlePheLeuHisIleIleIleThrMetThrGluValLeuTyrProVal 225

```


Db 121 GATCTGCTACTACCTGTTTTCACATCTCTTTTACACATTTGAAATGTATATCCAGTG 180
Qy 226 TyrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThrLeuMetLeuLeuThr 245
Db 181 CTCGTGATCTTAAAGTGTGATCTGCGAGTTTATCCAGGCTTTGTGTGATGTTTATGCC 240
Qy 246 CysLeuValTyrLeuLeuValSerTyrAlaHisThrSerTyrAspLeuArgSerLeu 265
Db 241 TGCATGTTTGGCTGAAGCTGTATCTTTTGACATACAAACCATGATATAGAAACCTG 300
Qy 266 AlaAsnAlaAlaAspLysAlaProGluValSer-----Tyr 278
Db 301 ATCAACGGCGCAAGAGTTGATATAGNACTACCGCGGCTGGCATAGATTAATTACAA 360
Qy 279 TyrValSerLeuLysSerLeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnPro 298
Db 361 GCTCCAACTCTTGGAGTCTAACATCTCATGATGGCTCCGACACTCTGTTATCCGCCA 420
Qy 299 SerTyrProArgSerAlaCysLeuArgLysGlyTyrValAlaArgGlnPheAlaLysLeu 318
Db 421 AGTATCTCTGAACACCTTATGTAGAAAGAGTTGGCTGGCTCCGTCACAGTTATCTACAC 480
Qy 319 ValIlePheThrGlyPheMetGlyPheIleGluSlnTyrIleAsnProIleValArg 338
Db 481 TTGATATTAATCTGCTCCAGGATTCATTTAGACATACATAAATCTTATCTGTTG 540
Qy 339 AsnSerIysHisProLeuLysGlyAspLeuLeuTyrAlaGluArgValLeuLysLeu 358
Db 541 AACTCTCAACATCCATTCGATGGAGGATTAAGTAAATGCTGTAGACACTGTTTGAAGTC 600
Qy 359 SerValProAsnLeuTyrValTyrLeuCysMetPheTyrCysPhePheHisLeuTrpLeu 378
Db 601 TCATACCAATGCTACTCTGGCTTTGCGAGTTTATGCTTTTTCATCTGCGGTA 660
Qy 379 AsnIleLeuAlaGluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsn 398
Db 561 AACATATCTGCTGAGATCTTCGATTTGCTGSCCGAGATTTCTACAAAGACTGGTGAA 720
Qy 399 AlaLysSerValGlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetVal 418
Db 721 GCAAAGACAAATGATGACTGCGAGAAAAGGAACATGCTGTGCATAAATGCAATGTT 780
Qy 419 ArgHisIleTyrPheProCysLeuArgSerLysIleProLysThrLeuAlaIleIle 438
Db 781 CGTCATATATATTTTCTTGATGCGAAATGGTATATCAAGAAAGTGTCTGTTTATA 840
Qy 439 AlaPheLeuValSerAlaVal-Phe----- 446
Db 841 TCGTTCCTTTGTTCTGCTGCTTTCATGAGTAACTTATTTTACCTTCTTCANCT 900
Qy 446 ----- 446
Db 901 GCATATATTAATATATAGTTCTCTATTTTCAAATGTGCTCTTCGAGTTTCGACATGCT 960
Qy 446 ----- 446
Db 961 TTTGTTCAAACCTTACCAGCTGTAGATTACTTGGATGAAGTGTCTATATATAAATTCATA 1020
Qy 447 -----HisG 448
Db 1021 TTTCAATCCAGTCCCTTTCGAGAAATATATACATTTTGTGATTTGTACACCA 1080
Qy 448 uLeuCysIleAlaValProCysArgLeuPheLysLeuTrpAlaPheLeuGlyIleMetPh 468
Db 1081 GTTATGCGTTCAGTTCCTCCGACATACTCAAAGTCTGGGCTTCTTAGGAATCATGCT 1140
Qy 468 eGlnValProLeuValPheIleThrAsnTyrLeuGlnGluArgPheGlySerThr---Va 487
Db 1-41 TCAGATTCCTCATATATGACATCATACTCAAAATTAATATTCAGTGACACCAATGCT 1200
Qy 487 lGlyAsnMetIlePheTrpPheIlePheCysIlePheGlyGlnProMetCysValLeuLe 507

Db 1201 TGGCAATATGATCTTTTGGTTTTTTTCTGCATATACGGCAGCAATGTGTCTTATT 1260
Qy 507 uTyrTyrHisAspLeuMetAsnArg 515
Db 1261 GTATTACCATGATGTGATGACCGG 1285
RESULT 13
US-10-223-076-16
? Sequence 16, Application US/10223076
? Publication NO. US20030074695A1
? GENERAL INFORMATION:
? APPLICANT: Paresse, Robert V
? TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
? TITLE OF INVENTION: Uses Thereof
? FILE REFERENCE: UCAL-105CIP3
? CURRENT APPLICATION NUMBER: US/10/223,076
? CURRENT FILING DATE: 2001-10-29
? PRIOR APPLICATION NUMBER: 10/040,315
? PRIOR FILING DATE: 2001-10-29
? PRIOR APPLICATION NUMBER: 09/339,472
? PRIOR FILING DATE: 1999-06-23
? PRIOR APPLICATION NUMBER: 60/107,771
? PRIOR FILING DATE: 1998-11-09
? PRIOR APPLICATION NUMBER: PCT/US98/17883
? PRIOR FILING DATE: 1998-08-28
? PRIOR APPLICATION NUMBER: 09/103,754
? PRIOR FILING DATE: 1998-06-24
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 16
? LENGTH: 1181
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 235, 236, 237, 238, 239, 317, 318, 319, 320, 321, 322, 393,
? LOCATION: 394, 395, 396, 397, 398
? OTHER INFORMATION: n = A,T,C or G
US-10-223-076-16
Alignment Scores:
Pred. No.: 6,66e-111 Length: 1181
Score: 1067.50 Matches: 192
Percent Similarity: 79.71% Conservative: 28
Best Local Similarity: 69.57% Mismatches: 47
Query Match: 38.52% Indels: 9
DB: 15 Gaps: 3
US-09-623-514A-2 (1-520) x US-10-223-076-16 (1-1181)
Qy 253 ValSerTyrAlaHisThrSerTyrAspIleArgSerLeuAlaAsnAlaAlaAspLys--- 271
Db 12 GTCTCTTATGCATACACAAATTTATGATATAGGGTATTGTCCAAAGTACTGAGAGGT 71
Qy 272 -----AlaAsnProGluValSerTyrTyrValSerLeuLysSerLeu 285
Db 72 GCTGCAATGGAATTTATGTCGATCTGAGATATGAAAGATCCACCTTTAAAGTCTA 131
Qy 286 AlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAlaCys 305
Db 132 GTGTACTTTCATGTTGGCCCAACACTCTTTGTACAGCAACCTTATCTCTCAAACTACATCT 191
Qy 306 IleArgLysGlyTyrValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPheMet 325
Db 192 ATTAGAAGGGTGGGTGACCCAGCAACTCATAAAAGTGGTGGNNNNNACAGCTTGATG 251
Qy 326 GlyPheIleGluGlnTyrIleAsnProIleValArgAsnSerIysHisProLeuLys 345
Db 252 GCCTTCATATGAGCAATATATAACCAATTTGAGAGAAATTCAAACATCCACCTGAAA 311
Qy 346 GlyAspLeuLeuTyrAlaIleGluArgValLeuLysLeuSerValProAsnLeuTyrVal 365

312 GGGANNNNNGAATGCTATAGAAAGAGCTTTAAAACTCTCAGTCGCCAACATTATATGTA 371
 QY TtpLeuCyMetPheTyrCysPhePheHisLeuTtpLeuAsnIleLeuAlaGluLeuLeu 385
 Db TGGCTTGTGATGTTCTATTGCGNNNNNCATTTATGGCTGAACATTTAGTGAACCTCTC 431
 QY CysPheGlyAspArgGluPheTyrLysAspTtpTtpAsnAlaLysSerValGlyAspTyr 405
 Db TGTTCGGTGACGGTGAATCTATAGAGACTGGTGGAAATGCCAAACTGTTGAGAGTAC 491
 QY TtpArgMetTtpAsnMetProValHisLysTtpMetValArgHisIleTyrPepProCys 425
 Db TGGAGGATGTGAACATGCTGTTTCAATAAGTGGATCATCAGACACATATATTTTCCATGT 551
 QY LeuArgSerLysIleProLysThrLeuAlaIleIleIleAlaPheLeuValSerAlaVal 445
 Db ATAAGAAAGAGCTTTTCCAGGGGTGAGCTATTCTAATCTCGTTCTGTTTTCAGCTGA 611
 QY PheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeuTtpAlaPheLeuGly 465
 Db TTCCATGAATATGATTATGGGTGGCGTGGCCACATTTTCAATCTGGGCATTTTCTGGG 671
 QY IleMetPheGluValProLeuValPheIleThrAsnTyrLeuGlnIleuArgPheGlySer 485
 Db ATCATGTTTCAGATACCGTTGGTATTCTTGACAAGATATCTCCATGCTACGTTCAAGCAT 731
 QY Thr---ValGlyAsnMetIlePheTtpPheIlePheCysIlePheGlyGlnProMetCys 504
 Db GTAATGGTGGGCAACATGATATTTTGGTTC---TTCAGTATAGTCGGACAGCGCATGTGT 788
 QY ValLeuLeuTyrTyrHisAspLeuMetAsnArgLysGlySerMetSer 520
 Db GTCTCTCTATACTACCATGATGATGACAGCAGCAGCGGCCCGCCAGT 836

RESULT 14

US-10-278-733-2
 ; Sequence 2, Application US/10278733
 ; Publication No. US20030100480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Steven
 ; APPLICANT: Chen, Robert
 ; APPLICANT: Farese, Robert V Jr
 ; TITLE OF INVENTION: Methods and compositions for modulating
 ; TITLE OF INVENTION: sebaceous glands
 ; FILE REFERENCE: USAL-105CIP4
 ; CURRENT APPLICATION NUMBER: US/10/278, 733
 ; CURRENT FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: 10/040,315
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 09/339,472
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/107,771
 ; PRIOR FILING DATE: 1998-11-09
 ; PRIOR APPLICATION NUMBER: PCT/US98/17883
 ; PRIOR FILING DATE: 1998-08-28
 ; PRIOR APPLICATION NUMBER: 09/103,754
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1467
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1467)
 ; OTHER INFORMATION: Homo sapiens diacylglycerol O-acyltransferase
 ; OTHER INFORMATION: homolog 1
 US-10-278-733-2

Alignment Scores: 2.47e-79 Length: 1467
 Pred. No.: 791.50 Matches: 194
 Score:

Percent Similarity: 53.14% Conservative: 77
 Best Local Similarity: 38.04% Mismatches: 174
 Query Match: 28.56% Indels: 65
 DB: 15 Gaps: 17
 US-09-623-514a-2 (1-520) x US-10-278-733-2 (1-1467)
 QY 25 ArgLeuArgArgLysSerArgSerAspSerSerAsnGlyLeuLeuLeuSerGlySer 44
 Db CGCGCGCGAGGACAGGGTGGCGGCTCGAGCCACCGCGGC----- 63
 QY 45 AspAsnAsnSerProSerAspValGlyValAlaProAlaAspValArgAspArgIleAsp 64
 Db -----GGCGGCGCTGGCGCGCGGAGAGAG----- 90
 QY 65 SerValValAsnAspAspAlaGlnGly---ThrAlaAsnLeuAlaGlyAspAsnAsnGly 83
 Db -----GTGCGGACCGCGCTGGCGGCGCCCGAGCGTGGAGCGCGGGGACCGGCCAGCC 144
 QY 84 GlyGlyAspAsnAsnGlyGlyGlyArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 103
 Db CGCGCGCGCCCAACAGACGAGACGCGCGCGTGGCGAGCGGCCACTGGAGCTGAGGTGC 204
 QY 104 ThrPheThrTyrArgProSerValProAlaHisArgAlaArgGluSerProLeuSer 123
 Db -----CATGCGCTGCAGGATTCTTTATTTCAGC 231
 QY 124 SerAspAlaIlePheLysGlnSerHisAlaGlyLeuPheAsnLeuCysValValValLeu 143
 Db TCTGACATGGGCTTC---AGCACTACCGTGGATCTCTGAACCTGGTGTGGTGGTATCTG 288
 QY 144 IleAlaValAsnSerArgLeuIleIleGluAsnLeuMetLysTyrGlyTtpLeuIleArg 163
 Db ATCTCAGCAATGCCCGGTATTCTTGGAGAACTCATCAAGTATGCACTCTGGTG--- 345
 QY 164 ThrAspPheTtpPheSerArgSerLeuArgAsp-----TtpProLeuPheMet 180
 Db GACCCCATCCAGGTGGTTCCTCTGTCTTCTGAGGATCCCTATAGCTGGCGCGCCCATGC 405
 QY 181 CysCysIleSerLeuSerIlePheProLeuAlaAlaPheThrValGluLysLeuValLeu 200
 Db CTGGTTATTGGCGCCAAATGCTTTGTGTGGCTGCACTCCAGGTGAGAGCGCCCTCGCG 465
 QY 201 GlnLysTyrIleSerGluProValIlePheLeuHisIleIleIleThrMetThrGlu 220
 Db GTGGTGGCTGACGAGCGGCGGAGCTGCTGTCACCTGGCCACCTGGCCACCAT 525
 QY 221 ValLeuTyrProValTyrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThr 240
 Db CTGTGTTCCACGCGCTGTGTCTTACTGGTTCAGTCTATCACTCCAGTGGGCTCCCTG 585
 QY 241 LeuMetLeuLeuThr---CysIleValTtpLeuLysLeuValSerTyrAlaHisThrSer 259
 Db CTGGCGCTGATGGCGCACACCATCTCTCTTCTCAAGCTCTTCTCTACCGC----- 636
 QY 260 TyrAspIleArgSer-----LeuAlaAsnAlaAlaAspLys 271
 Db ---GACGTCAACTCATGCTGCGCGCGCGCCAGGCGCTGCTCTGCGAGGAGAG 693
 QY 272 AlaAsnPro-----GluValSerTyr-----TyrValSerLeuLysSer 284
 Db GCCAGCAGTGTCTGCTGCCCGCGCACACCGTGAAGTACCGCGGACAACTCTGACCTACCGGAT 753
 QY 285 LeuAlaTyrPheMetValAlaProThrLeuCysTyrGlnProSerTyrProArgSerAla 304
 Db CTCTACTTCTCTCTTTCGCGCCCGCCCTGTGTGCTACGAGCTCAACTTTCGCGCTCTCCC 813
 QY 305 CysIleArgLysGlyTtpValAlaArgGlnPheAlaLysLeuValIlePheThrGlyPhe 324
 Db CGCATCGGAGCGCTTCTGCTGCGAGCGATCCTTGAGATGCTGTCTTCAACCAGCTC 873
 QY 325 MetGlyPheIleIleGluGlnTyrIleAsnProIleValArgAsnSerLysHisProLeu 344


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Db      814 CGCATCCGGAGCGCTTCTGCTGCGACGATCCCTTGAGATGCTGTCTTCCACCCAGCTC 873
QY      325 MetGlyPheIleIleGluGlnTyrIleAsnProIleValArgAsnSerLysHisProLeu 344
Db      874 CAGGTGGGGCTGATCCAGCAGTGGATGTCCTCCACCATCCAGAACTCCATGAAGCCCTTC 933
QY      345 LysGlyAspLeuLeuTyrAla-----IleGluArgValIleLysSerValProAsn 362
Db      934 AAG--GACATGGACTACTCAGCATCAGAGCGCTCTCTGAAGTGGGGTCCCAAT 990
QY      363 LeuTyrValTrpLeuCysMetPheTyrCysPhePheHisLeuTrpLeuAsnIleLeuAla 382
Db      991 CACCTCATCTGCTCATCTCTCTACTGCTCTTCCACTCCTGCTGCTGAATGCCGTGCT 1050
QY      383 GluLeuLeuCysPheGlyAspArgGluPheTyrLysAspTrpTrpAsnAlaLysSerVal 402
Db      1051 GAGCTCATGAGTTTGGAGACCGGAGTTCTACCGGAGCTGGTGGAACTCCGAGTCTGTC 1110
QY      403 GlyAspTyrTrpArgMetTrpAsnMetProValHisLysTrpMetValArgHisIleTyr 422
Db      1111 ACCTACTTCTGGCAGAACTGGAACTCCCTCTGTGCACAGTGGTGCATCAGACACTTCTAC 1170
QY      423 PheProCysLeuArgSerLysIleProLysThrLeuAlaIleIleLeuAlaPheLeuVal 442
Db      1171 AAGCCCATGCTTCGACGGGCGACAGCAAGTGGATGCCAGGACACGGGTGTTCTCTGGCC 1230
QY      443 SerAlaValPheHisGluLeuCysIleAlaValProCysArgLeuPheLysLeuTrpAla 462
Db      1231 TCGGCTTCTTCCACGAGTACTCTGGTGGAGCTCCTCTGCGAATGTTCCGCTCTGGGCT 1290
QY      463 PheLeuGlyIleMetPheGlnValProLeuVal---PheIleThrAsnTyrLeuGlnGlu 481
Db      1291 TTCACGGGCATGATGGCTCAGATCCCACTGGCTGGTTCGTGGCGCGCTTTTCCAGGGC 1350
QY      482 ArgPheGlySerThrValGlyAsnMetIlePheTrpPheIlePheCysIlePheGlyGln 501
Db      1351 AACTAT-----GSCAAGCAGCTGTGTGG---CTGTGCTCATCATCGGACAG 1395
QY      502 ProMetCysValLeuLeuTyrTyrHisAsp 511
Db      1396 CCAATAGCGCTCCTCATGTACTGTCACGAC 1425
```

Search completed: May 5, 2004, 21:38:15
Cdb time : 580 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 11:32:37 ; Search time 130.654 Seconds
(without alignments)
8087.241 Million cell updates/sec

Title: US-09-623-514A-1

Perfect score: 1904

Sequence: 1 attcttagttcttcttc.....ttatgtgtaagcgccgc 1904

Scoring table: IDENTITY NUC

Gapop 15°C, Gapext 1.0

Searched: 632709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1839.4	96.6	1942	4	US-09-326-203A-1
2	1125.4	59.1	1512	4	US-09-593-359-3
3	954	50.1	1446	4	US-09-593-359-1
4	336.4	17.7	629	4	US-09-103-754A-3
5	141.8	7.4	1650	4	US-09-103-754A-2
6	141.2	7.4	1976	3	US-09-165-042-2
7	139.6	7.3	1895	4	US-09-326-203A-14
8	137.6	7.2	1766	4	US-09-326-203A-15
9	137.6	7.2	1765	4	US-09-326-203A-16
10	125.8	6.6	275	4	US-09-326-203A-5
11	122.6	6.4	234	4	US-09-326-203A-3
12	123.4	5.7	254	4	US-09-326-203A-8
13	109.4	5.7	254	4	US-09-313-294A-580
14	108.2	5.7	267	4	US-09-326-203A-4
15	123.6	5.4	262	4	US-09-326-203A-9
16	103.6	5.4	262	4	US-09-313-294A-1662
17	93	4.9	325	4	US-09-326-203A-7
18	68.4	3.6	325	4	US-09-326-203A-10
19	57	3.0	4011	1	US-08-121-057-3
20	57	3.0	4011	2	US-08-509-187D-3
21	57	3.0	4011	2	US-09-121-396-3
22	57	3.0	4011	5	PCT-US93-09704A-3
23	57	3.0	4079	1	US-08-121-057-2
24	57	3.0	4079	2	US-08-509-187D-2
25	57	3.0	4079	2	US-09-121-396-2
26	57	3.0	4079	5	PCT-US93-09704A-2
27	55.8	2.9	519	4	US-09-326-203A-11

28	52.2	2.7	1607	4	US-09-328-857A-1	Sequence 1, Appli
29	51.6	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
30	50	2.6	1509	4	US-09-328-857A-2	Sequence 2, Appli
31	50	2.6	2040	3	US-09-165-042-4	Sequence 4, Appli
32	49	2.6	518	4	US-09-326-203A-12	Sequence 12, Appl
33	43	2.3	18596	3	US-09-318-448-11	Sequence 11, Appl
34	43	2.3	18597	4	US-09-962-665-8	Sequence 8, Appli
35	43	2.3	18597	4	US-09-963-333-8	Sequence 8, Appli
36	39.2	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
37	37.4	2.0	399	4	US-09-621-976-8976	Sequence 8976, Ap
38	36.4	1.9	288	4	US-09-119-507B-111	Sequence 111, App
39	36.4	1.9	288	4	US-09-547-693-111	Sequence 111, App
40	36.2	1.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
41	36.2	1.9	834	4	US-09-621-976-2574	Sequence 2574, Ap
42	36.2	1.9	1813	4	US-09-620-312D-29	Sequence 29, Appl
43	36.2	1.9	3821	4	US-08-956-171B-304	Sequence 304, App
44	35.6	1.9	248	3	US-09-007-005-32	Sequence 32, Appl
45	35.6	1.9	248	3	US-09-244-796-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-326-203A-1
; Sequence 1, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Laesner, Mike
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1942
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-326-203A-1

Query Match	96.6%	Score	1839.4	DB	4	Length	1942	
Best Local Similarity	99.9%	Pred. No.	0					
Mismatches	1840	Conservative	0	Mismatches	1	Indels	0	Gaps
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Db	99	ATTCTTAGCTTCTTCTTCTTCAATCCGCTCTTTCCCTCTCCCATAGATTCTGTTCTCTT	158					
QY	61	TCAATTCTCTGCGATGCTCTGATCTCTCTGAGGCTCTTCTCCGAGCTGTTT	120					
Db	159	TCAATTCTCTGCGATGCTCTGATCTCTCTGAGGCTCTTCTCCGAGCTGTTT	218					
QY	121	CGTCAAAAGCTTTTTCGAAATGGCGATTTCGATCTCTGCTGGCGTTTACTACGGTACGGAG	180					
Db	219	CGTCAAAAGCTTTTTCGAAATGGCGATTTCGATCTCTGCTGGCGTTTACTACGGTACGGAG	278					
QY	181	AACGGTGGCGGAGATTCTGTCATCTTCTGATAGCTTCGTCGCGGAATCGATCGGAT	240					
Db	279	AACGGTGGCGGAGATTCTGTCATCTTCTGATAGCTTCGTCGCGGAATCGATCGGAT	338					
QY	241	TCTCTTACGAGCTTCTTCTCTCTGTTCCGATAATAATCTCTCGATGATGTTGTA	300					
Db	339	TCTCTTACGAGCTTCTTCTCTCTGTTCCGATAATAATCTCTCGATGATGTTGTA	398					
QY	301	GCTCCGCGCGAGCTTAGGGATCGGATTGATTCGGTGTGTTAAAGATGAGCTCAGGAAACA	360					

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Db 339 GCTCCGCGGAGCTTAGGATCGGATTTGATTCGGTTGTTAAAGATGACGCTCAGGGAACA 458
 QY 361 GCCAATTTGGCCGAGATAAATAACGGTGGTGGCGATAATAACGGTGGTGGAGAGCGGC 420
 Db 459 GCCAATTTGGCCGAGATAAATAACGGTGGTGGCGATAATAACGGTGGTGGAGAGCGGC 518
 QY 421 GGAG 480
 Db 519 GGAG 578
 QY 481 CGGAGGCGGAG 540
 Db 579 CGGAGGCGGAG 638
 QY 541 TTTTTCACCTCTGTGTAGTAGT 600
 Db 639 TTTTTCACCTCTGTGTAGTAGT 698
 QY 601 CTATGAGAGATGTTGGTGTGATCAGAACGATTTCTGGTTTGTAGTTCAAGATCGGTGCGA 660
 Db 699 CTATGAGAGATGTTGGTGTGATCAGAACGATTTCTGGTTTGTAGTTCAAGATCGGTGCGA 758
 QY 661 GATTTGGCCGCTTTTTCATGT 720
 Db 759 GATTTGGCCGCTTTTTCATGT 818
 QY 721 GTTGAGAAATTTGGT 780
 Db 819 GTTGAGAAATTTGGT 878
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 Db 999 TATGCTCATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
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 QY 1201 GTGTGAACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1260
 Db 1299 GTGTGAACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1358
 QY 1261 CACCTTTGGTAAACATATGTCAGAGCTTCTCTGCTTGGGATCGTGAATCTCAAA 1320
 Db 1359 CACCTTTGGTAAACATATGTCAGAGCTTCTCTGCTTGGGATCGTGAATCTCAAA 1418
 QY 1321 GATTTGTGAAATGCAAAAAGTGTGGAGATTTACTGAGAGATGGAATATGCTTTTCAT 1380
 Db 1419 GATTTGTGAAATGCAAAAAGTGTGGAGATTTACTGAGAGATGGAATATGCTTTTCAT 1478
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 Db 1479 AAATGGATGTTTGCACATATATCTTTCCCGTGTCTGCGAGCAAGATACCAAGACATC 1538

QY 1441 GCCATTATCATTTCTTCT 1500
 Db 1539 GCCATTATCATTTCTTCT 1598
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 QY 1621 ATCTTCTGCTATTTCTGCAACCGATGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
 Db 1719 ATCTTCTGCTATTTCTGCAACCGATGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1778
 QY 1681 CGAAAGAGATCGATGTCATGAACAACTGTTCAAAAATGACCTTTCTCTCAACATCTATG 1740
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 QY 1741 GCTCTGTTGATCTCCGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800
 Db 1839 GCTCTGTTGATCTCCGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1898
 QY 1801 ATAAACATTTGAAGAAAGAAAGAAATTTAGAGTTGTTGTTATC 1841
 Db 1899 ATAAACATTTGAAGAAAGAAAGAAATTTAGAGTTGTTGTTATC 1939
 RESULT 2
 US-09-593-359-3
 ; Sequence 3, Application US/09593359
 ; Patent No. 6552250
 ; GENERAL INFORMATION:
 ; APPLICANT: Laroche, Andre J.
 ; APPLICANT: Kykforuk, Cory L.
 ; APPLICANT: Weselake, Randall J.
 ; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
 ; FILE REFERENCE: 24015050
 ; CURRENT APPLICATION NUMBER: US/09/593,359
 ; CURRENT FILING DATE: 2000-06-14
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO. 3
 ; LENGTH: 1512
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; OTHER INFORMATION: DGAT1
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1512)
 US-09-593-359-3
 Query Match 59.1%; Score 1125.4; DB 4; Length 1512;
 Best Local Similarity 84.5%; Pred. No. 0;
 Matches 1321; Conservative 0; Mismatches 191; Indels 51; Gaps 3;
 QY 139 ATGCGCATTTTGAATTTCTGCTGCGGTACTACCGTGAACGAGAACGTTGGCGGAGTTTC 198
 Db 1 ATGCGCATTTTGAATTTCTGAGCGCTGCTGTACCOCGACGGAGAACGGCG-----TC 54
 QY 199 GTCGATCTTGATAGGCTTCGTTCGACGAAATCGAGATCGGATTTCTTAAACGACATTTCT 258
 Db 55 GCGGATCTCGACAGGCTTCACCGTCGTAATCGAGTTGCGATTTCTTCAACGACATCTTC 114
 QY 259 CTCTCTGTTTCCGATATAATTTCTCTCTCGATGATGTTTGGAGCTCCCGCGGACGTTAGG 318
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 QY 319 GATCGGATTTGATTCGGTTGTTTAAAGATGACGCTCAGGAAACAGCCATTTGGCGGAGAT 378
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 Db 223 GATCGCGAAACTAGGGAATCCGCGGAGG----- 251
 QY 439 GCCGATCTACGTTTACGTATCGACCGTGGGTCCAGTCTATCGAGGGCGGAGAGAGT 498
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 QY 1699 TGA 1701
 Db 1510 TGA 1512

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 US-09-593-359-1
 ; Sequence 1, Application US/09593359
 ; Patent No. 6552250
 ; GENERAL INFORMATION:
 ; APPLICANT: Iaroché, Andre J.
 ; APPLICANT: Nykiforuk, Cory D.
 ; APPLICANT: Weselake, Randall J.
 ; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
 ; FILE REFERENCE: 24015US0
 ; CURRENT APPLICATION NUMBER: US/09/593,359
 ; CURRENT FILING DATE: 2000-06-14
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1446
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; OTHER INFORMATION: DCAT2
 ; NAME/KEY: CDS
 ; LOCATION: (82)..(1107)
 US-09-593-359-1

Query Match 50.1%; Score 954; DB 4; Length 1446;
 Best Local Similarity 91.8%; Pred. No. 2.1e-28;
 Matches 1019; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

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 Db 300 GGTTCCTTATGCTCTATCTAGCTATGATTAAGATTCCTAGCAATGACGCTGATAAGGC 359

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QY 360 CAATCTGAGTCTCTACTAGTTAGCTTGAAGAGCTTGCATATTTTCATGTCGTCC 419
DB |||||
QY 1014 CACATGTTGTTATCAGCCAAAGTTATCCAGTCTCTCATGTATACGGAAGGTTGGGTGC 1073
DB |||||
QY 420 CACATGTTGTTATCAGCCAAAGTTATCCAGTCTCTCATGTATCCGGAAGGTTGGGTGC 479
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QY 480 TCGTCAATTTGCAAACTGGTTCATATTTACCTGGACTCATGGGATTTAATAGACAATA 539
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QY 1134 TATAATCTTATGTCAGAACTCAAGCATCTTTGAAGGGATCTTCTATATGCTAT 1193
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QY 540 TATAATCTTATGTTAGAACTCAAGCATCTCTGAAGGGGACCTTCTATATGCTAT 599
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QY 1194 TGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGCTCTGCACTTCTACTG 1253
DB |||||
QY 600 TGAAGAGTGTGAAGCTTTCAGTTCCAAATCTATATGTGTGGCTCTGCACTTCTACTG 659
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QY 1254 CTTCTTCCACCTTTGGTTAAACATATTTGGCAGAGCTTCTCTGCTTGGGGATCGTAAT 1313
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QY 660 CTTCTTCCACCTTTGGTTAAACATATTTGGCAGAGCTTCTCTGCTTGGGGATCGTAAT 719
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QY 1314 CTACAAAGATTCGTGGAATGCAAAAGTGTGGAGATTTACTGGAGATGTGGAATATGTC 1373
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QY 720 CTACAAAGATTCGTGGAATGCAAAAGCTTGGAGATTTATGGAGATGTGGAATATGTC 779
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QY 1374 TGTTCATAAATGGATGGTTTCGACATATATPACTTCCGTCCTTGGCAGCAAGATACCAA 1433
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QY 780 TGTTCATAAATGGATGGTTTCGACATATATPACTTCCGTCCTTGGCAGCAAGATACCAA 839
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QY 1434 GACATCTGCCATATCATGCTTCTCTAGTCTCTGAGTCTTCTATGATGATGATGCTG 1493
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QY 1494 AGTCTCTGCTCTCTCAAGCTATGGCTTCTTCTGGGATATGTTTCAGTGTCTTT 1553
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QY 900 AGTCTCTGCTCTCTCAATCTATGGCTTCTATGGGATATGTTTCAGTGTCTTT 959
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QY 1614 CTGTTCTATCTCTGATTTTGGACACCGATGCTGCTCTTATATACAGACCT 1673
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QY 1080 GATGAACCGAAAGGATGATGCTATGAAA 1109
DB |||||
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RESULT 4

US-09-103-754A-3

; Sequence 3, Application US/09103754A

; Patent No. 6344548

; GENERAL INFORMATION:

; APPLICANT: Fares, Robert

; APPLICANT: Cases, Sylvaine

; APPLICANT: Smith, Steven

; APPLICANT: Erickson, Sandra

; TITLE OF INVENTION: Diacylglycerol O-acyltran

; TITLE OF INVENTION: sferase

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESS: Bozicevic & Reed

; STREET: 285 Hamilton Avenue, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,754A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 6510-105p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650 327 3400
; TELEFAX: 650 327 3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-754A-3
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Query Match 17.7%; Score 336.4; DB 4; Length 629;

Best Local Similarity 94.8%; Pred. No. 1e-92;

Matches 381; Conservative 0; Mismatches 16; Indels 5; Gaps 3;

QY 1047 TGCATGATACGAGAGGTTGGTGGCTGCTCAATTTGCAAACTGGTTCATATTCACCG 1106

DB 1 TGCATGATACGAGAGGTTGGTGGCTGCTCAATTTGCAAACTGGTTCATATTCACCG 60

QY 1107 ATTCAATGGATTTATAATAGAAACAATATAAATCCTATTGTCAAGAACTCAAGCATCC 1166

DB 61 ATTCAATGGATTTATAATAGAAACAATATAAATCCTATTGTCAAGAACTCAAGCATCC 120

QY 1167 TTTGAAAGCGATCTCTATATGCTATTTGAAAGAGTGTGAAGCTTTCAGTTCCAAATTT 1226

DB 121 TTTGAAAGCGATCTCTATATGCTATTTGAAAGAGTGTGAAGCTTTCAGTTCCAAATTT 180

QY 1227 ATATCTGTGCTCTGATGCTCTATGCTCTTCCACCTTTTCCACCTTTTAAACATATTCGAGA 1286

DB 181 ATATCTGTGCTCTGATGCTCTATGCTCTTCCACCTTTTCCACCTTTTAAACATATTCGAGA 240

QY 1287 GCTTCTCTGCTTCCGGGATCGTGAATTTCTACAAAGATTTGCTGGAATSCAAAAGTGTGG 1346

DB 241 GCTTCTCTGCTTCCGGGATCGTGAATTTCTACAAAGATTTGCTGGAATSCAAAAGTGTGG 300

QY 1347 AGATTACT--GGAGATGTGGAATATGCTGTTTCATAAATGG--ATGTTTCGACATATATA 1403

DB 301 AGATTACTGGAGATGTGGAATATGCTGTTTCATAAATGGATGGTTCGACATATATA 360

QY 1404 C--TTCCCGTCTCCGACAGATACCAAGACATCGCC 1443

DB 361 CTTCCCGTCTCCGACAGATACCAAGACATCGCC 402

RESULT 5

US-09-103-754A-2

; Sequence 2, Application US/09103754A

; Patent No. 6344548

; GENERAL INFORMATION:

; APPLICANT: Fares, Robert

; APPLICANT: Cases, Sylvaine

; APPLICANT: Smith, Steven

; APPLICANT: Erickson, Sandra

; TITLE OF INVENTION: Diacylglycerol O-acyltran

; TITLE OF INVENTION: sferase

; NUMBER OF SEQUENCES: 6

RESULT 7

US-09-326-203A-14
; Sequence 14, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Lasser, Mike
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: m:sc feature
; LOCATION: (209)
; OTHER INFORMATION: n at position 209 is unknown
US-09-326-203A-14

Query Match 7.3%; Score 139.6; DB 4; Length 1895;
Best Local Similarity 54.0%; Pred. No. 3.3e-32;
Matches 308; Conservative 0; Mismatches 259; Indels 3; Gaps 1;
QY 997 TATTTCATGTCGCTCCACATTTGTGTATCAGCCAAAGTTATCCAGTTTCGTCATGTATA 1056
Db 705 TACTTCTCTCTGCCCCACCTTGTGTACGAGCTCAACTTTCGCCGCTCTCCCGCATC 764
QY 1057 CGAAGGGTTGGTGCTCGTCAATTTGCAAACTGGTGTATTTACCGGATTCATGGGA 1116
Db 765 CGAAGCGCTTCTGCTCGAAGGATCTTGAAGTCTGTCTTCCACCCAGCTCCAGTG 824
QY 1117 TTATTAATGAACAATATATAATCTTATTTGAGAACTCAAGCACTCTTTGAAGGC 1176
Db 825 GGGCTGATCCAGCAGTGATGTCCTCCACCATCCAGAACTCCATGAAGCCCTTCAAGGAC 884
QY 1177 ----GATCTCTATATGCTATTGAAGAGTGTGAAGCTTCAGTTCCAAATTTATATGTG 1233
Db 885 ATGACTACTCACGCAATCATCGAGCGCTCTCTGAAGCTGGCGGTCCCAATCACTCATC 944
QY 1234 TGCGCTTGCAATGTTCTACTGCTCTTCCACCTTTGGTTAAACATATTGGCAGAGCTTCTC 1293
Db 945 TGCTTCATCTTCTTCTACTGGCTCTTCCACTCTGCTGATGTCGCTGGTGGCTGAGTCATG 1004
QY 1294 TGCTTCGGGATCGTGAATTTCTACAAAGATTGTTGGAATGCAAAAGTTGGGAGATTAC 1353
Db 1005 CAGTTTGGAGACCGGAGTTTCTACCGGAGCTGGTGAATCTCCGAGTCTGTCACTTCTC 1064
QY 1354 TGGAGATGTGAATATGCTGTCTATATATGATGTTGATGATGTTGATATATATATATAT 1413
Db 1065 TGGCAGAACTGGAACATCTCCCTGTGTCACAAAGTTGGTATCAGACACTTCTCAAGCCCATG 1124
QY 1414 TTGGCAGCAAGATACCAAGACACTCGCCATTTATCTTCTTCTTCTTCTTCTTCTTCTTCT 1473
Db 1125 CTTTCAGCGGAGCAGCAAGTGGATGGCCAGCAGCGGTGTCTTCTGGCTCGGCCCTC 1184
QY 1474 TTTTCATGAGCTATGCAATCGAGTTCTTGTCTGTCTTCTTCAAGCTATGGGCTTTTCTTGGG 1533
Db 1185 TTTCCAGAGTACCTGGTGGAGCTCCCTCTCGAATGTTCCGCTCTCTGGGCTTTCACGGGC 1244
QY 1534 ATTATGTTTCAGGTGCTTTGGTCTTTCATC 1563
Db 1245 ATGATGGCTCAGATCCCACTGGCTGGTTC 1274

1563

RESULT 8

US-09-326-203A-15
; Sequence 15, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Lasser, Mike
; APPLICANT: Ruzinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1766
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-326-203A-15

Query Match 7.2%; Score 137.6; DB 4; Length 1766;
Best Local Similarity 53.6%; Pred. No. 1.3e-31;
Matches 309; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
QY 997 TATTTCATGTCGCTCCACATTTGTGTATCAGCCAAAGTTATCCAGTTTCGTCATGTATA 1056
Db 834 TACTTCACTTCTGCTCTACTTGTGTATGAACCTCAACTTTCCTGATCCCGCCGAATA 893
QY 1057 CGAAGGGTTGGTGCTCGTCAATTTGCAAACTGGTGTATTTACCGGATTCATGGGA 1116
Db 894 CGAAGCGCTTCTGCTGACGGGGTCTTGTGAGTGTCTTTTTCACCCAGCTTCAGTG 953
QY 1117 TTATTAATGAACAATATATAATCTTATTTGAGAACTCAAGCACTCTTTGAAGGC 1176
Db 954 GGGCTGATCCAGCAGTGATGTCCTCTACTATCCAGAACTCCATGAAGCCCTTCAAGGAC 1013
QY 1177 ----GATCTCTATATGCTATTGAAGAGTGTGAAGCTTTCAAGTTCCAAATTTATATGTG 1233
Db 1014 ATGACTATTTCAAGAACTCATTGAGCGTCTCTTAAAGCTGGCGGTCCCAACCATCTGATA 1073
QY 1234 TGCGCTTGCAATGTTCTACTGCTCTTCCACCTTTGGTTAAACATATTGGCAGAGCTTCTC 1293
Db 1074 TGCTTCATCTTCTTCTACTGGCTTTTCCACTCATGTCTCAATGCTGGCAGAGCTCTCTG 1133
QY 1294 TGCTTCGGGATCGTGAATTTCTACAAAGATTGTTGGAATGCAAAAGTTGGGAGATTAC 1353
Db 1134 CAGTTTGGAGACCGGAGTTCTACAGGAGCTGGTGAATGCTGAGTCTGTCACTACTTT 1193
QY 1354 TGGAGATGTGAATATGCTGTCTATATATGATGTTGATGATGTTGATATATATATATATAT 1413
Db 1194 TGGCAGAACTGGAATATCCCGCTGTGCAAGTGGTGCATCAGACACTTCTCAAGCCCATG 1253
QY 1414 TTGGCAGCAAGATACCAAGACACTCGCCATTTATCTTCTTCTTCTTCTTCTTCTTCTTCT 1473
Db 1254 CTGAGCTGGGAGCAACAATGATGGCCAGAGCTGGGCTCTTTTGGGCTCAGCCCTC 1313
QY 1474 TTTTCATGAGCTATGCAATCGAGTTCTTGTCTGTCTTCTTCAAGCTATGGGCTTTTCTTGGG 1533
Db 1314 TTCCATGAGTACCTAGTGGAGCAATTTCCCTCGAGGATGTTCCGCTCTGCGCTTTCAGAGCC 1373
QY 1534 ATTATGTTTCAGGTGCTTTGGTCTTTCATCACAAC 1569
Db 1374 ATGATGGCTCAGGTCCCACTGGCTGGATTTGTGAAC 1409

RESULT 9

US-09-326-203A-16
; Sequence 16, Application US/09326203A
; Patent No. 6444876

Query Match 6.4%; Score 122.6; DB 4; Length 234;
Best Local Similarity 75.3%; Pred. No. 1.4e-27;
Matches 177; Conservative 0; Mismatches 56; Indels 2; Gaps 2;
QY 976 GTTAGCTTCAAGAGCTTGCATATTTTCATGGTCGCTCCCA-CATTTGTGTTATCAGCCAAG 1034
DB 1 GTAAGCTTCAAGAGCTTACATANTYCTGGTGGTCCCTTANCAATTATGTTACAGCCAAN 60
QY 1035 TTATCCACGTTTCGATGATATACGGAAGGTTGGTGGCTGGTCAATTTGCAAACTGGT 1094
DB 61 CTATCTCGCACACCTTATATTCGAAAGGTTGGCTGGTTCGCAACTTG-TCAACTGAT 119
QY 1095 CATATTCCAGGATTCATGGGATTTATATAGCAATATATAAATCCTATTGTCAGGA 1154
DB 120 AATATTTACAGGAGTTATGGGATTTATATAGCAATATATAAATCCTATTGTCAGGA 179
QY 1155 CTCAAAGCATCTTTGAAAGGCGATCTTCTATATGCTATTGAAAGAGTGTGAAG 1209
DB 180 TTCACAGCATCTCTCAAGGAAACCTTCTTACGCCATCGAGAGATTCTGAAG 234

RESULT 12
US-09-326-203A-8
Sequence 8, Application US/09326203A
Patent No. 6444876
GENERAL INFORMATION:
APPLICANT: Lasser, Mike
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 8
TYPE: DNA
ORGANISM: Zea mays
US-09-326-203A-8

Query Match 5.7%; Score 109.4; DB 4; Length 254;
Best Local Similarity 65.2%; Pred. No. 1.6e-23;
Matches 161; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 605 TGAAGTATGGTTGGTTGATCAGAAAGGATTTCTGGTTTAGTTCAAGATCGCTGCGAGATT 664
DB 1 TGAAGTATGGCTTATTAAATAGATCTGGCTTTGGTTTAAATGCTACATCATTCGCGAGACT 60
QY 665 GCGCGCTTTTCATGCTGTATATCCCTTTTCGATCTTCCCTTTGGCTGCTTTTACGGTTG 724
DB 61 GGCCACTGCTAATGCTTGCCTTAGCTACCCATATTTCCCTTTGGTGCATTTGCGAGCTG 120
QY 725 AGAATTTGCTACTTCAGAAATACATATCAGAACTGTTGTCATCTTCTTCATATTATTA 784
DB 121 AAAAGTTGGCAATTCACAAATCTCATTAGTATGATCTGCTACTACTCTTTTTCATCTTT 180
QY 785 TCACCATGACAGAGTTTGTATCCAGTTTATCCAGTTTACCTACCCCTAAGTGTGATTCGCTTTT 844
DB 181 TTACAACATTTGAATTTGATATCCAGTCTCGTGATCTTTAAGTGTGATTCGCGATT 240
QY 845 TATCAGG 851
DB 241 TATCAGG 247

RESULT 13
US-09-313-294A-580

Sequence 580, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalugudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 580
LENGTH: 254
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700549471H1
US-09-313-294A-580

Query Match 5.7%; Score 109.4; DB 4; Length 254;
Best Local Similarity 65.2%; Pred. No. 1.6e-23;
Matches 161; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 605 TGAAGTATGGTTGGTTGATCAGAAAGGATTTCTGGTTTAGTTCAAGATCGCTGCGAGATT 664
DB 1 TGAAGTATGGCTTATTAAATAGATCTGGCTTTGGTTTAAATGCTACATCATTCGCGAGACT 60
QY 665 GCGCGCTTTTCATGCTGTATATCCCTTTTCGATCTTCCCTTTGGCTGCTTTTACGGTTG 724
DB 61 GGCCACTGCTAATGCTTGCCTTAGCTACCCATATTTCCCTTTGGTGCATTTGCGAGCTG 120
QY 725 AGAATTTGCTACTTCAGAAATACATATCAGAACTGTTGTCATCTTCTTCATATTATTA 784
DB 121 AAAAGTTGGCAATTCACAAATCTCATTAGTATGATCTGCTACTACTCTTTTTCATCTTT 180
QY 785 TCACCATGACAGAGTTTGTATCCAGTTTATCCAGTTTACCTACCCCTAAGTGTGATTCGCTTTT 844
DB 181 TTACAACATTTGAATTTGATATCCAGTCTCGTGATCTTTAAGTGTGATTCGCGATT 240
QY 845 TATCAGG 851
DB 241 TATCAGG 247

RESULT 14
US-09-326-203A-4
Sequence 4, Application US/09326203A
Patent No. 6444876
GENERAL INFORMATION:
APPLICANT: Lasser, Mike
APPLICANT: Ruzitsky, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: DNA
ORGANISM: Glycine max
US-09-326-203A-4

Query Match 5.7%; Score 108.2; DB 4; Length 267;
Best Local Similarity 67.0%; Pred. No. 3.9e-23;
Matches 179; Conservative 0; Mismatches 68; Indels 20; Gaps 1;


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QY      836 CTGCTTTTCTTCAAGTGTGCACITTTGATCTCTCACTGCAITGTGTGGCTAAAGTTGG 895
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QY      896 TTCTTTATGCTCATATAGTCTATGACATAGATCCCTAGCCCAATGCCAGCTGATAAGG--- 952
Db      61 TGTCAATGACATACAACTATGATATGAGAGCACTTACTGTTCGATCGAATGAAGGGAG 120

QY      953 -----CCATCTCTGAAGTCTCTACTACGTTAGCTTTGAAGAGCTTGGC 995
Db      121 AAACATTACCCCAATCTTATGATATGAGATATCCCTACACTGTGACCTTACGAGTTGGC 180

QY      996 ATATTTTCATGCTGCTCCCATTTGTGTATCAGCCAGTTATCCAGTTCTTGCAATGAT 1055
Db      181 ATACTTCTGTTGCTCTCTACATTTATGCTATCAGCAGCTATCTCTGCACACCTTCAGT 240

QY      1056 ACGAAGGTTGGTGGCTCGTCAATT 1382
Db      241 TCGAAGGTTGGTGTTCGTCAACT 257
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RESULT 15

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US-09-326-203A-9
; Sequence 9, Application US/09326203A
; Patent No. 6444676
; GENERAL INFORMATION:
; APPLICANT: Lassar, Mike
; APPLICANT: Ruzizinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 9
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Zea mays
US-09-326-203A-9
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Query Match      5.4%; Score 103.6; DB 4; Length 262;
Best Local Similarity 63.0%; Pred. No. 9.9e-22;
Matches 160; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
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QY      606 GAAGTATGGTGTGATCAGACGGATTCTGCTTTAGTTCAAGATCGCTGCGAGATTG 665
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QY      666 GCGGCTTTTCATGTTGTATATCCCTTTGATCTTTTGGCTGGCTTTACGGTTGA 725
Db      61 GCCACTCTATGTTGCTTGCCTTACTACCATATTTCCCTTGGTGCATTTGCACTCGA 120

QY      726 GAAATGGTACTTCAGAAATACATATACAGAACCTGTTGTCTATCTTTCTCATATATAT 785
Db      121 AAAGTTGGCAATCAACAATCTCATAGTAGATCTGCTACTACCTGTTTTCACATCCCTTT 180

QY      786 CACCATGACAGAGGTTTGTATCCAGTTTACGTCACCTACGTTGATCTGCTTTT 845
Db      181 TACAACATTTGAATTTATATCCAGTCTCGTATCTTTAAGTGTGATCTCGAGTTT 240

QY      846 ATCAGGTGTCACTT 859
Db      241 ACAGGCTTTGTGT 254
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Title: US-09-623-514A-1

Perfect score: 1904

Sequence: 1 attcttagctctctcttc.....ttatgggtgaagggcgcc 1904

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Searched: 2936184 seqs, 2261732022 residues

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Post-processing: Minimum Match 0%

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Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1146.4	60.2	1537	15	US-10-223-076-4
4	1125.4	59.1	1512	15	US-10-223-076-8
5	954	50.1	1446	15	US-10-223-076-6
6	751.6	39.5	2090	15	US-10-223-076-10
7	702.4	36.9	1621	13	US-10-425-114-10163
8	702.4	36.9	1888	13	US-10-424-599-111496
9	697	36.5	2099	15	US-10-223-076-12
10	692	36.3	1964	15	US-10-223-076-14
11	470	24.7	470	9	US-09-770-444-209
12	379.4	19.9	1572	15	US-10-223-076-17
13	371	19.5	380	9	US-09-770-791-192
14	365.6	19.2	1181	15	US-10-223-076-16

15	336.4	17.7	629	15	US-10-273-438-4	Sequence 4, Appli
16	336.4	17.7	629	15	US-10-223-076-1	Sequence 1, Appli
17	336.4	17.7	629	15	US-10-040-315A-4	Sequence 4, Appli
18	336.4	17.7	629	17	US-10-659	Sequence 4, Appli
19	332.8	17.5	1150	16	US-10-260-238-310	Sequence 310, App
20	269.6	14.2	827	13	US-10-425-114-13703	Sequence 13703, A
21	239.4	12.6	362	13	US-10-424-599-115051	Sequence 115051, A
22	237.6	12.5	775	13	US-10-424-599-68382	Sequence 68382, A
23	154.2	8.1	1035	16	US-10-369-493-30171	Sequence 30171, A
24	154.2	8.1	1497	15	US-10-278-733-5	Sequence 5, Appli
25	151.4	8.0	798	13	US-10-425-114-6719	Sequence 6719, Ap
26	145	7.6	1497	15	US-10-278-733-1	Sequence 1, Appli
27	145	7.6	1497	15	US-10-278-733-12	Sequence 12, Appli
28	144.2	7.6	1698	15	US-10-278-733-6	Sequence 6, Appli
29	141.8	7.4	1650	15	US-10-273-438-3	Sequence 3, Appli
30	141.8	7.4	1650	15	US-10-273-438-9	Sequence 9, Appli
31	141.8	7.4	1650	15	US-10-040-315A-3	Sequence 3, Appli
32	141.8	7.4	1650	15	US-10-040-315A-9	Sequence 9, Appli
33	141.8	7.4	1650	17	US-10-659-800-3	Sequence 3, Appli
34	141.8	7.4	1650	17	US-10-659-800-9	Sequence 9, Appli
35	141.2	7.4	1467	15	US-10-278-733-9	Sequence 9, Appli
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37	139.6	7.3	1411	15	US-10-273-438-1	Sequence 1, Appli
38	139.6	7.3	1411	15	US-10-040-315A-1	Sequence 1, Appli
39	139.6	7.3	1411	17	US-10-659-800-1	Sequence 1, Appli
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42	137.6	7.2	1497	15	US-10-278-733-3	Sequence 3, Appli
43	137.6	7.2	1766	14	US-10-157-855-15	Sequence 15, Appli
44	137.6	7.2	1766	14	US-10-157-855-16	Sequence 16, Appli
45	135.2	7.1	893	13	US-10-424-599-25340	Sequence 25340, A

ALIGNMENTS

RESULT 1

US-10-223-076-2
; Sequence 2, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)...(1701)
US-10-223-076-2

Query Match 100.0%; Score 1904; DB 15; Length 1904;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1904; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
61 TCAATCTCTCTGATCTCTCTGATCTCTCTGAGCTCTTCTTCCCGAGCTGTTT 120
QY 121 CGTCAAAAGCTTTTCAAAATGGGATTTGGATCTGCTGGCGTTACTAGGTGAGGAG 180
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121 CGTCAAAAGCTTTTCAAAATGGGATTTGGATCTGCTGGCGTTACTAGGTGAGGAG 180
QY 181 AACGGTGGCGGAGATCTGCGATCTTGTAGAGCTTGTGTCAGCGAAATCGAGATCGGAT 240
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181 AACGGTGGCGGAGATCTGCGATCTTGTAGAGCTTGTGTCAGCGAAATCGAGATCGGAT 240
QY 241 TCTTCTAAAGGACTTCTCTCTCTGCTTCCGTAATAAATCTCTTCCGATGATTTGGA 300
DB |||||
241 TCTTCTAAAGGACTTCTCTCTCTGCTTCCGTAATAAATCTCTTCCGATGATTTGGA 300
QY 301 GCTCCGCGCGAGCTTAGGATCTGATGATTCGTTGTTAAAGATGACGCTCAGGAGACA 360
DB |||||
301 GCTCCGCGCGAGCTTAGGATCTGATGATTCGTTGTTAAAGATGACGCTCAGGAGACA 360
QY 361 GCCAATTTGGCCGGAGATAATAACGGTGTGGGATTAATAACGGTGTGGAGAGCGGC 420
DB |||||
361 SCCAATTTGGCCGGAGATAATAACGGTGTGGGATTAATAACGGTGTGGAGAGCGGC 420
QY 421 GAGAGAGGAGAGAAACCGCGATGTPACGTTTACGATCGACCGTCCGTTCCAGCTCAT 480
DB |||||
421 GAGAGAGGAGAGAAACCGCGATGTPACGTTTACGATCGACCGTCCGTTCCAGCTCAT 480
QY 481 CGAGAGCGGAGAGAGTCCACTTAGCTCCGAGCAATCTTCAACAGAGCCATCGCGGA 540
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DB |||||
541 TTAATCAACCTCTGTGTAGTCTTATATGCTGTAACAGTAGTACATCATCGAAAT 600
QY 601 CTTAAGAGATGTTGTTGATCAGAACGGATTTCTGTTTGTAGTCAAGATCGCTCGGA 660
DB |||||
601 CTTAAGAGATGTTGTTGATCAGAACGGATTTCTGTTTGTAGTCAAGATCGCTCGGA 660
QY 661 GATGCGCGCTTTTCACTGTGTATATCCCTTTCGATCTTCTTGGCTGCTTTACG 720
DB |||||
661 GATGCGCGCTTTTCACTGTGTATATCCCTTTCGATCTTCTTGGCTGCTTTACG 720
QY 721 GTGAGAAATTTGGTACTTCAGAAATACATATCAGAACTGTGTCTCTTCTCATATT 780
DB |||||
721 GTGAGAAATTTGGTACTTCAGAAATACATATCAGAACTGTGTCTCTTCTCATATT 780
QY 781 ATTATCAGATGACAGAGTTTGTATCCAGTTTACGTCACCTTAAGGTGTATCTGCT 840
DB |||||
781 ATTATCAGATGACAGAGTTTGTATCCAGTTTACGTCACCTTAAGGTGTATCTGCT 840
QY 841 TTTTATCAGGTGTCTTTGATGCTCTCTCACTTGCATTTGTGCTTAAAGTTGTTTCT 900
DB |||||
841 TTTTATCAGGTGTCTTTGATGCTCTCTCACTTGCATTTGTGCTTAAAGTTGTTTCT 900
QY 901 TATGCTCATAGTATGATAGATCCCTAGCCAAATCGAGCTGATAGAGCCAAATCTCT 960
DB |||||
901 TATGCTCATAGTATGATAGATCCCTAGCCAAATCGAGCTGATAGAGCCAAATCTCT 960
QY 961 GAAGTCTCTACTAGTTAGCTTGAAGAGCTTGGCATATTTTATGCTCCAGATTG 1020
DB |||||
961 GAAGTCTCTACTAGTTAGCTTGAAGAGCTTGGCATATTTTATGCTCCAGATTG 1020
QY 1021 TGTATCAGCAAGTTATCAAGTCTCTGATGTATAGAGAGGTTGGGTGGCTCGTCAA 1080
DB |||||
1021 TGTATCAGCAAGTTATCAAGTCTCTGATGTATAGAGAGGTTGGGTGGCTCGTCAA 1080
QY 1081 TTTGCAAACTGGTCTATATTCAACGGATTCATGGGATTTATATAGAACAAATATATAAT 1140

DB |||||
1081 TTTGCAAACTGGTCTATATTCAACGGATTCATGGGATTTATATAGAACAAATATATAAT 1140
QY 1141 CTTATTTGTCAGAACTCAAGAGCATCTTTGAAAGGCGATCTTCTATATGCTATTTGAAAGA 1200
DB |||||
1141 CTTATTTGTCAGAACTCAAGAGCATCTTTGAAAGGCGATCTTCTATATGCTATTTGAAAGA 1200
QY 1201 GTGTTGAAGCTTTCAAGTCTCAAAATTTATATGTTGGCTCTGCAATTTCTACTGCTTCTTC 1260
DB |||||
1201 GTGTTGAAGCTTTCAAGTCTCAAAATTTATATGTTGGCTCTGCAATTTCTACTGCTTCTTC 1260
QY 1261 CACCTTTGGTTAAACATATTGGCAGAGCTTCTCTGCTTCGGGATCTGGAATTTCAAAA 1320
DB |||||
1261 CACCTTTGGTTAAACATATTGGCAGAGCTTCTCTGCTTCGGGATCTGGAATTTCAAAA 1320
QY 1321 GATTTGGGAATGCAAAAGTGTGGGAGATTAATGAGAAATGTGGAATATGCTGCTTCAT 1380
DB |||||
1321 GATTTGGGAATGCAAAAGTGTGGGAGATTAATGAGAAATGTGGAATATGCTGCTTCAT 1380
QY 1381 AAATGAGTGGTTCGACATATATATCTCCCTGCTTGGCAGAGATACCAAGACACTC 1440
DB |||||
1381 AAATGAGTGGTTCGACATATATATCTCCCTGCTTGGCAGAGATACCAAGACACTC 1440
QY 1441 GCCATTTATCATTTGCTTTCTTAGTCTCTGCACTCTTTCATGAGCTATGCTGCGATTCCT 1500
DB |||||
1441 GCCATTTATCATTTGCTTTCTTAGTCTCTGCACTCTTTCATGAGCTATGCTGCGATTCCT 1500
QY 1501 TGTGCTCTCTTCAAGCTATGCGCTTTTCTTGGGATTTATGTTTCAAGTCTGCTTGGCTTC 1560
DB |||||
1501 TGTGCTCTCTTCAAGCTATGCGCTTTTCTTGGGATTTATGTTTCAAGTCTGCTTGGCTTC 1560
QY 1561 ATCAAACTATCTACAGGAAAGTGTGGCTCAACCGTGGGAAACATGATCTTCTGGTTC 1620
DB |||||
1561 ATCAAACTATCTACAGGAAAGTGTGGCTCAACCGTGGGAAACATGATCTTCTGGTTC 1620
QY 1621 ATCTTCTGCATTTTCGACCAACCGATGTGTGCTCTTTTATTACCAGACCTGATGAAC 1680
DB |||||
1621 ATCTTCTGCATTTTCGACCAACCGATGTGTGCTCTTTTATTACCAGACCTGATGAAC 1680
QY 1681 GAAAGGATCGATGCTCATGAAACAACTGTTCAAAAATGACTTTCTCAACATCTATG 1740
DB |||||
1681 GAAAGGATCGATGCTCATGAAACAACTGTTCAAAAATGACTTTCTCAACATCTATG 1740
QY 1741 GCCTCGTTCATCTCCCTTCATGTTGTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB |||||
1741 GCCTCGTTCATCTCCCTTCATGTTGTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 ATAACTTGAAGAGAAAGAAATTTAGAGTTGTTGATCTGCAAAAATTTTGGTAGAG 1860
DB |||||
1801 ATAACTTGAAGAGAAAGAAATTTAGAGTTGTTGATCTGCAAAAATTTTGGTAGAG 1860
QY 1861 ACAGCAAACTGGTTCGATTTTGTATGTTGTTAAAGCGCGCG 1904
DB |||||
1861 ACAGCAAACTGGTTCGATTTTGTATGTTGTTAAAGCGCGCG 1904

RESULT 2

US-10-157-855-1
; Sequence 1, Application US/10157855
; Publication No. US20020170091A1
; GENERAL INFORMATION:
; APPLICANT: Lussner, Michael W.
; APPLICANT: Ruzhinskiy, Diane M.
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: -6516.158
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/10/157,855
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,399

; PRIOR FILING DATE: 1998-11-12
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 1
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-10-157-855-1

Query Match 96.6%; Score 1839.4; DB 14; Length 1942;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1840; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATTTCTAGCTTCTTCTCAATCGGCTCTTCCCTCTCCATAGATCTCTTCTTCTT	60
DB	99	ATTTCTAGCTTCTTCTCAATCGGCTCTTCCCTCTCCATAGATCTCTTCTTCTT	158
QY	61	TCAATTTCTTCTGATGCTTCTGATCTCTCTGACGCTCTTTTCTCCGACGCTTTT	120
DB	159	TCAATTTCTTCTGATGCTTCTGATCTCTCTGACGCTCTTTTCTCCGACGCTTTT	218
QY	121	CGTCAACGCTTTTCGAAATGGCGATTTTGAATCTGCTGGCGTTACTACGGTACGGAG	180
DB	219	CGTCAACGCTTTTCGAAATGGCGATTTTGAATCTGCTGGCGTTACTACGGTACGGAG	278
QY	181	AACGGTGGCGAGAGTTGCTCGATCTTGTATAGGCTTGTGACGCGAATCGAGATCGGAT	240
DB	279	AACGGTGGCGAGAGTTGCTCGATCTTGTATAGGCTTGTGACGCGAATCGAGATCGGAT	338
QY	241	TCCTTCAACGACCTTCTTCTCTGGTTCGGATTAATTTCTCTCGATGATGTTGGA	300
DB	339	TCCTTCAACGACCTTCTTCTCTGGTTCGGATTAATTTCTCTCGATGATGTTGGA	398
QY	301	GCTCCGCGACCTTAGGATCGATGATTTCCGTTGTAAAGATGACGCTCAGGGAACA	360
DB	399	GCTCCGCGACCTTAGGATCGATGATTTCCGTTGTAAAGATGACGCTCAGGGAACA	458
QY	361	GCAATTTGCGCGAGATTAATACGGTGTGGCGATTAATTAACGGTGGGAGAGCGGC	420
DB	459	GCAATTTGCGCGAGATTAATACGGTGTGGCGATTAATTAACGGTGGGAGAGCGGC	518
QY	421	GGAGAAGAAAGAGAAACGCCGATGCTACGTTTACGATCGACGCTCGGTTCCAGCTCAT	480
DB	519	GGAGAAGAAAGAGAAACGCCGATGCTACGTTTACGATCGACGCTCGGTTCCAGCTCAT	578
QY	481	CGAGGGCGAGAGAGTCCATTTAGCTCCGACGCAATCTTCAACAGAGCGATGCGGGA	540
DB	579	CGAGGGCGAGAGAGTCCATTTAGCTCCGACGCAATCTTCAACAGAGCGATGCGGGA	638
QY	541	TTATTCAACCTCTGTGTAGTATTTCTTATTCCTGTAACAGTACGATCATCATCGAAAT	600
DB	639	TTATTCAACCTCTGTGTAGTATTTCTTATTCCTGTAACAGTACGATCATCATCGAAAT	698
QY	601	CTTATGAAGTATGGTTGATGATCAGAACGGAATTTCTGGTTAGTTCAGATCGCTGGA	660
DB	699	CTTATGAAGTATGGTTGATGATCAGAACGGAATTTCTGGTTAGTTCAGATCGCTGGA	758
QY	661	GATTTGGCGCTTTTCAATGTTGTATATCCCTTTCGATCTTTCCTTGGCTGCGCTTACG	720
DB	759	GATTTGGCGCTTTTCAATGTTGTATATCCCTTTCGATCTTTCCTTGGCTGCGCTTACG	818
QY	721	GTTGAGAAATTTGTTACTTCAGAAATACATATCGAACCTGTGTATCTTCTTCATATT	780
DB	819	GTTGAGAAATTTGTTACTTCAGAAATACATATCGAACCTGTGTATCTTCTTCATATT	878
QY	781	ATTATCCCATGACAGAGGTTTGTATCCAGTTTACGTCACCCCTAAGGTGTGATCTGCT	840
DB	879	ATTATCCCATGACAGAGGTTTGTATCCAGTTTACGTCACCCCTAAGGTGTGATCTGCT	938
QY	841	TTTTTATCAGGTTCACCTTTCATGCTCTCTCATTTGCTTAAAGTTGGTTTCT	900
DB	939	TTTTTATCAGGTTCACCTTTCATGCTCTCTCATTTGCTTAAAGTTGGTTTCT	998

QY	901	TATGCTCATCTAGCTATGACATAGATCCCTAGCAATGAGCTGTATAAGGCCAATCTCT	960
DB	999	TATGCTCATCTAGCTATGACATAGATCCCTAGCAATGAGCTGTATAAGGCCAATCTCT	1058
QY	961	GAAGTCTCTCTACTAGCTTGAAGAGCTTGGCATATTTTCATGGTCCCTCCCATTTG	1020
DB	1059	GAAGTCTCTCTACTAGCTTGAAGAGCTTGGCATATTTTCATGGTCCCTCCCATTTG	1118
QY	1021	TGTTATCAGCCCAAGTTATCCAGCTTCTGCATGTATACGAGAGGTTGGTGGCTGTCNA	1080
DB	1119	TGTTATCAGCCCAAGTTATCCAGCTTCTGCATGTATACGAGAGGTTGGTGGCTGTCNA	1178
QY	1081	TTTGCMAAATCTGGTCAATATTCACCGGATTCATGGGATTTATAATAGAACATATATAAT	1140
DB	1179	TTTGCMAAATCTGGTCAATATTCACCGGATTCATGGGATTTATAATAGAACATATATAAT	1238
QY	1141	CCTATTGTCAGAACTCAAGCATCTTTGAAAGCGATCTTCTATATGCTATTGAAAGA	1200
DB	1239	CCTATTGTCAGAACTCAAGCATCTTTGAAAGCGATCTTCTATATGCTATTGAAAGA	1298
QY	1201	GTGTGAGAGCTTTCAGTTCCGAATTTATATCTGTGGCTCTGCATGTTCTACTGCTTCTC	1260
DB	1299	GTGTGAGAGCTTTCAGTTCCGAATTTATATCTGTGGCTCTGCATGTTCTACTGCTTCTC	1358
QY	1261	CACCTTTGGTTTAAACATATTTGCGAGGCTTCTCTGCTTCCGGGATCGTGAATTTCTACAAA	1320
DB	1359	CACCTTTGGTTTAAACATATTTGCGAGGCTTCTCTGCTTCCGGGATCGTGAATTTCTACAAA	1418
QY	1321	GATTGGTGGAAATGCAAAAGTGTGGGATTAATCTGAGAAATGTGAATATGCTGTTCAAT	1380
DB	1419	GATTGGTGGAAATGCAAAAGTGTGGGATTAATCTGAGAAATGTGAATATGCTGTTCAAT	1478
QY	1381	AAATGGATGGTTCGACATATATATCTCCGCTGCTGCGACGATACCAAGACATCTC	1440
DB	1479	AAATGGATGGTTCGACATATATATCTCCGCTGCTGCGACGATACCAAGACATCTC	1538
QY	1441	GCCATTATCATTTGCTTCTAGTCTCTGAGTCTTTCATGAGCTATGATCGCAGTTCTCT	1500
DB	1539	GCCATTATCATTTGCTTCTAGTCTCTGAGTCTTTCATGAGCTATGATCGCAGTTCTCT	1598
QY	1501	TGTCGTCTCTTCAAGCTATGGGCTTTTCTTGGGATTTATGTTTCAGGTGCTTTGGTCTTTC	1560
DB	1599	TGTCGTCTCTTCAAGCTATGGGCTTTTCTTGGGATTTATGTTTCAGGTGCTTTGGTCTTTC	1658
QY	1561	ATCCAACTATCTACAGAAAGTGTGGCTCAACGGTGGGAAATCATGATCTTCTGGTTC	1620
DB	1659	ATCCAACTATCTACAGAAAGTGTGGCTCAACGGTGGGAAATCATGATCTTCTGGTTC	1718
QY	1621	ATCTTCTGCAATTTTCGACCAACCGATGTGTGTCTTCTTTATACCAAGCTGATGAAC	1680
DB	1719	ATCTTCTGCAATTTTCGACCAACCGATGTGTGTCTTCTTTATACCAAGCTGATGAAC	1778
QY	1681	CGAAAGGATCGATGTCATGAAACAACTGTTTCAAAAATGACTTTCTTCAAACTATG	1740
DB	1779	CGAAAGGATCGATGTCATGAAACAACTGTTTCAAAAATGACTTTCTTCAAACTATG	1838
QY	1741	GCCTCGTGGATCTCCGTTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1800
DB	1839	GCCTCGTGGATCTCCGTTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1898
QY	1801	ATAACCATTTGAAGAGAAAGAAATTTAGAGTTGTTGTATC	1841
DB	1899	ATAACCATTTGAAGAGAAAGAAATTTAGAGTTGTTGTATC	1939

RESULT 3
 US-10-223-076-4
 ; Sequence 4, Application US/10223076
 ; Publication No. US20030074695A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Farese, Robert V
 ; APPLICANT: Cases, Sylvaine
 ; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and

```

; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1537
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1107)
US-10-223-076-4

Query Match      60.2%; Score 1146.4; DB 15; Length 1537;
Best Local Similarity 86.1%; Pred. No. 0;
Matches 1350; Conservative 0; Mismatches 161; Indels 57; Gaps 5;

QY 132 TTTCGAATGCGGATTTGGATTTCTGCTGGCTTACTACGGTGACGGAGAAACGGTGGCGG 191
DB 15 TTTCGAATGCGGATTTGGATTTCTGCTGGCTTACTACGGTGACGGAGAAACGGTGGCGG 74
QY 192 AGAGTTGCTGCATCTTGATAGGCTTCTGTCAGCGAAATCGAGATCGGATTTCTTAACGG 251
DB 75 -----CGATCTCGATACGCTTCTGTCAGCGAAACCGAGATCGGATTTCTTAACGG 125
QY 252 ACTTCTTCTCTGCTGGTTCGGAATTAATCTCTCTCGGATGATTTGGAGCTCCGCGA 311
DB 126 ACTTCTTCTCTGCTGGTTCGGAATTAATCTCTCTCGGATGATTTGGAGCTCCGCGA 161
QY 312 CTTTGGGATCGGATTTGATTTGCTGTTTAAACGATGACGCTCAGCGAAACAGCAATTTGGC 371
DB 162 CGTGGAGGATCGGTTGATTTGATCTGCTT---GAGGATCTCAGGAAAGCAATTTGGC 218
QY 372 CGGAGATTAATACGGTGGTGGCGATTAATACGGTGGTGGAGGCGCGGAGAGGAAG 431
DB 219 CGGAG-----AAACGAAATTTAGGGAATCGGTTGGAGAGCGGG 257
QY 432 AGGAAACGCGGATGCTAGCTTTACGATATCGACGCTGGTTTCCAGCTCATCGGAGGCGGAG 491
DB 258 GGGAAACGTTGGATGATGAGGTACAGTATCGGCGCTCGCTTCAGCTCATCGGAGGTCG 317
QY 492 AGAGAGTCCATTTAGCTTCGAGCGCAATCTTCAAACAGAGCCATGCGGATTTATCAACCT 551
DB 318 GAGAGATCCACTCAGCTCTGAGCGCCATCTTCAAACAGAGCCATGCTGAGCTATTCACCT 377
QY 552 CTGCTGATGATCTTTATTTGCTGTAAGAGTATGATCATCATCGAATCTTATGAGTA 611
DB 378 GTGTGTAGTGTCTTGTGTCTGTAAGAGTATGATCATCATCGAATCTTATGAGTA 437
QY 612 TGGTTGGTTGATCAGAAAGGATTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 671
DB 438 CGGTTGGTTGATCAGAAAGGATTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 497
QY 672 TTTCATGTTGTTATATCCCTTTTGCATCTTCTTCTTGGCTTTCGCTTTTACGTTTGAATTT 731
DB 498 TTTCATGTTGTTATATCCCTTTTGCATCTTCTTCTTGGCTTTCGCTTTTACGTTTGAATTT 557
QY 732 GGTACTTCAAAATCATATCAGAACTGTTGTCATCTTCTTCTTCAATATTAATTAATCAACAT 791
DB 558 AGTACTTCAAAATGATATCTGAACCTGTTGTCATCTTCTTCTTCAATATTAATTAATCAACAT 617

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QY 792 GACAGAGTTTGTATCCAGTTTACGTCACCCCTAAGGTGTGATCTGCTTTTATCAGG 851
DB 618 GACCGAGGTTTGTATCCAGTTTACGTCACCCCTAAGGTGTGATCTGCTTTTATCAGG 677
QY 852 TGTCACTTTGATGCTCTCTCAGTTTGCATTTGCTGCTTAAAGTTTGGTTTCTTATGCTATAC 911
DB 678 TGTCACTTTGATGCTCTCTCAGTTTGCATTTGCTGCTTAAAGTTTGGTTTCTTATGCTATAC 737
QY 912 TAGCTATGATATGATGCTCTCTCAGTTTGCATTTGCTGCTTAAAGTTTGGTTTCTTATGCTATAC 971
DB 738 TAACTATGATATGATGCTCTCTCAGTTTGCATTTGCTGCTTAAAGTTTGGTTTCTTATGCTATAC 797
QY 972 CTACGTTTACCTTGAAGAGCTTTGCGATATTTTCACTGCTGCTTCCACATTTGTTATCAGCC 1031
DB 798 CTATGTTTACCTTGAAGAGCTTTGCGATATTTTCACTGCTGCTTCCACATTTGTTATCAGCC 857
QY 1032 AAGTTTATCCAGCTTTGCTGATGATATAGCGAAGGTTTGGTGGCTCGTCAATTTTCAAAACT 1091
DB 858 GAGCTATCCAGCTTTTCCATGATATCCGGAAGGTTTGGTGGCTCGTCAATTTTCAAAACT 917
QY 1092 GGTCAATATTCACCGGATTTATATAGGATTTATATAGAACATATATATAATCTTATGTCAG 1151
DB 918 GATCAATATTCACCGGATTTATATAGGATTTATATAGAACATATATATAATCTTATGTCAG 977
QY 1152 GAACTCAAAAGCATCTTTGAAAGCGCATCTTCTATATGCTTATTTGAAAGAGTGTGGAAGCT 1211
DB 978 GAACTCAAAAGCATCTTTGAAAGCGCATCTTCTATAGCGGATTTCTTATAGCGGTTTGAAGAGTGTGGAAGCT 1037
QY 1212 TTCAGTTTCCAAATTTATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1271
DB 1038 TTCAGTTTCCAAATTTATATAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
QY 1272 AAACATATTTGGGAGAGCTTCTGCTTCCGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1331
DB 1098 AAACATATTTGGGAGAGCTTCTGCTTCCGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1157
QY 1332 TGCAAAAGCTGTTGGAGATTTACTGGAATATGCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1391
DB 1158 TGCAAAAGCTGTTGGAGATTTATGGAATATGCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217
QY 1392 TGCAATATATATCTTCCGCTGCTTGGCGAGCAAGATACCAAGACACTGCGCAATATATCAT 1451
DB 1218 TGCAATATATATCTTCCGCTGCTTGGCGAGCAATATACCAAGACACTGCGCAATATATCAT 1277
QY 1452 TGCTTCTTCTAGCTCTGCTGCTGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1511
DB 1278 TGCTTCTTCTAGCTCTGCTGCTGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337
QY 1512 CAAGCTATGCGGCTTTTCTTGGGATTTATGTTTCAAGGTGCTTGTGCTTCTTCAATCAAACTA 1571
DB 1338 CAAGCTATGCGGCTTTTCTTGGGATTTATGTTTCAAGGTGCTTGTGCTTCTTCAATCAAACTA 1397
QY 1572 TCTACAGGAAAGTTTGGCTTCAACGGTGGGGAACATGATCTTCTGCTTCAATCTTCTGCTAT 1631
DB 1398 CTTACAGGAAAGTTTGGCTTCAACGGTGGGGAACATGATATCTTCTGCTTCAATCTTCTGCTAT 1457
QY 1632 TTTTGGAGAACCGATGCTGCTTCTTCTTATTTACAGGCTGCTGATCAACCGAAAGGATC 1691
DB 1458 TTTTGGAGAACCGATGCTGCTTCTTCTTATTTATCAAGCTTGTATGATGATGATGATGATGAT 1517
QY 1692 GATGCTAT 1699
DB 1518 GATGCTAT 1525

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RESULT 4
 US-10-223-076-8
 ; Sequence 8, Application US/10223076
 ; Publication No. US20030074695A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Farese, Robert V
 ; APPLICANT: Cases, Sylvaine
 ; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and

;; TITLE OF INVENTION: Uses Thereof
;; FILE REFERENCE: UCAL-105CIP3
;; CURRENT APPLICATION NUMBER: US/10/223,076
;; CURRENT FILING DATE: 2001-10-29
;; PRIOR APPLICATION NUMBER: 10/040,315
;; PRIOR FILING DATE: 2001-10-29
;; PRIOR APPLICATION NUMBER: 09/339,472
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/107,771
;; PRIOR FILING DATE: 1998-11-09
;; PRIOR APPLICATION NUMBER: PCT/US98/17883
;; PRIOR FILING DATE: 1998-08-28
;; PRIOR APPLICATION NUMBER: 09/103,754
;; PRIOR FILING DATE: 1998-06-24
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 1512
;; TYPE: DNA
;; ORGANISM: Brassica napus
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(1512)
US-10-223-076-8

Query Match 59.1%; Score 1125.4; DB 15; Length 1512;
Best Local Similarity 84.5%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 191; Indels 51; Gaps 3;
QY 139 ATGCGATTTTGGATTCTGCTGGCTTACTAGCGTGACGGGAACGGTGGCGGAGAGTTC 198
DB 1 ATGCGATTTTGGATTCTGAGGSCCTGCTGTACCGCCGACGGAGACGGCG-----TC 54
QY 199 GTCGATCTGTAGAGCTTCGTGCGACGGAAATCGAGATCGGATCTCTPAAACGACTCTTT 258
DB 55 GCGGATCTCGACAGGCTCCACGGTGGTAAATCGAGTTCGGATCTCTCCAAACGACTCTCTC 114
QY 259 CTCCTGCTTCCGATAAATCTCTTCGGATGATGTTGGAGCTCCGCGACGCTTAGG 318
DB 115 TCCG-----ATACCTTCCCGTCCGACGATGTTGGAGCTGCGCGGCCGAAAGG 162
QY 319 GATCGGATGATTCGGTGTAAAGATGACGCTCAGGGAAACAGCCAAATTTGGCCCGGAGAT 378
DB 163 GATCGGTTGATTCGGCTGCCGAGGAGAGGCTCAGGGAAACAGCGAATTTAGCTGCGGA 222
QY 379 AATACGGTGTGGGATATAAAGCGTGTGGAAGAGCGCGGAGAGAGAGAAAC 438
DB 223 GATCCGAAACTAGGGAATCCGCGCGAGG----- 251
QY 439 GCGGATGCTACGTTTACGATGACCGCTCGTTCCAGCTCATCGGAGGCGAGAGAGT 498
DB 252 --CGATGTAAGTTTACGATGACCGCTCGTTCCAGCTCATCGGAGGACGAGGAGAGT 309
QY 499 CCACTAGCTCCGACGCAATCTTCAAAACAGAGGCCATGCGGATTAATCAACCTCTGTGTA 558
DB 310 CCACTAGCTCCGACGCTATCTTCAAAACAGAGGCCATGCGGATTAATCAACCTCTGTGTA 369
QY 559 GTAGTCTTATGCTGTAACAGTAGACTCATCATCGAAATCTTATGAAATGAGTTGG 618
DB 370 GTTGTCTTGTGTGTTAAACAGTAGACTCATCATCGAAATCTTATGAAATGAGTTGG 429
QY 619 TTGATCAGACGAGATTTCTGTTTGTAGTTTCAAGATGCTCGGAGATTCGCGCTTTTCATG 678
DB 430 TTGATCAGACTGATTTTGTGTTTGTAGTTTCAATCTTACAGACTGCGCGCTTTTCATG 489
QY 679 TGTGTATATCCCTTTCGATCTTTCTTGGCTGCTTTTACGTTTGAATAATTTGTACTT 738
DB 490 TGTGTCTTTCACCTTCGCTCTTCTTCTTGGCTGCTTTCAGCTCAGAAATGATGACTT 549
QY 739 CAGAAATACATATCAGAAACCTTGTGTCACTCTTCTTCATATATTATCACCATGACAG 798
DB 550 CAGAAATACATATCAGAAACCTTGTGTCACTCTTCTTCATATATTATCACCATGACAG 609

QY 799 GTTGTGATCCAGTTTACGTACACCTTAAGGCTGTGATTCGTCTTTTATCAGGTGTCAC 858
DB 610 GTCTTGTGATCCAGTCTACGTACACTGAGGTGTGATTCGTCTTTTATCAGGTGTCAC 669
QY 859 TTGATGCTCTCTCACTTGTGCTTAAAGTTTGGTTTCTTATCTCTATCTATAGCTAT 918
DB 670 TTGATGCTCTCTCACTTGTGCTTAAAGTTTGGTTTCTTATCTCTATCTATAGCTAT 729
QY 919 GACATAAGATCCCTAGCCTAGCCTGATAGGCAATCTCTGAACTCTCTCTACTAGTT 978
DB 730 GACATAAGAAACCTCTGCAATTTCACTGATAGGCTGATCTCTGAAATCTCTCTACTAGTT 789
QY 979 AGCTTGAAGAGCTTCGCAATTTCTATGCTCCACATTTGTTATCAGCCAAAGTTAT 1038
DB 790 AGCTTGAAGAGCTTCGCAATTTCTATGCTCCACACTGTGTTATCAGCCAAAGCTAT 849
QY 1039 CCACGTTCTGATGTATACGGAAGGTTGGGTGGCTCGTCAATTTTCAAACTGGTCTCA 1098
DB 850 CCACGTTCTGATGTATCCGGAAGGTTGGGTGGCTCGTCAATTTTCAAACTGGTCTCA 909
QY 1099 TTACCCGATTCATGGGATTTATATAGAAATATATATAATCTCTATCTCTAGGAACTCA 1158
DB 910 TTCACTGACTCATGGGATTTATATAGAGCAATATATAATCTCTATCTCTAGGAACTCA 969
QY 1159 AAGCATCTTTGAAAGGCGATCTTCTATATGCTATTTGAAGAGCTGTGAGCTTTTCACT 1218
DB 970 AAGCATCTTCTGAAAGGCGCTTCTATATGCTATTTGAAGAGCTGTGAGCTTTTCACT 1029
QY 1219 CCAAAATTTATATGCTGTGCTCTGCAATTTCTACTGCTTTTCCACCTTTGGTTTAAACATA 1278
DB 1030 CCAAAATTTATATGCTGTGCTCTGCAATTTCTACTGCTTTTCCACCTTTGGTTTAAACATA 1089
QY 1279 TTGGCAGAGCTTCTCTGCTTCCGCGATCTGTAATTTCTAAGAGTTGGTGGATGCAAAA 1338
DB 1090 TTGGCAGAGCTTCTCTGCTTCCGCGACCTGTAATTTCTAAGAGTTGGTGGATGCAAAA 1149
QY 1339 AGTGTGCGAGATTTACTGCGAATGTGGATATGCTGTTTCAATAAATGAGTTGGTGGAT 1398
DB 1150 AGCTTGGAGATTTTGGAGATGTGGAAATGCTCTGTTTCAATAAATGAGTTGGTGGAT 1209
QY 1399 ATATACCTTCCGCTGTGCGCAGCAAGATACCAAAAGACACTCGCCATTTATCTTCTTTC 1458
DB 1210 ATATACCTTCCGCTGTGCGCAGCAAGATACCAAAAGTACCGCCATTTATCTTCTTTC 1269
QY 1459 CTAGTCTCTGAGTCTTTCATGAGCTATGCAATCGAGTTCTTGTGCTCTCTTCAAGCTA 1518
DB 1270 CTAGTCTCTGAGTCTTTCATGAGTTATGCAATCGAGTTCTTGTGCTCTCTTCAATCTA 1329
QY 1519 TGGGCTTTTCTTGGGATTTATGTTTTCAGGTGCTTGTGCTTCTCATCAAACTATCTACAG 1578
DB 1330 TGGGCTTTTCTTGGGATTTATGTTTTCAGGTGCTTGTGCTTCTCATCAAACTATCTACAG 1389
QY 1579 GAAAGTTTGGCTCAACGCTGGGGAACATGATCTTCTGTTTCTCTTCTCTCTTCTTCTCGGA 1638
DB 1390 GAAAGTTTGGCTCAACGCTGGGGAACATGATCTTGTGTTTCTTGTGCTTCTTGTGCTTCTCGGA 1449
QY 1639 CAACCGATGTGTGCTCTTCTTATACAGAGCTGATGAAACGAAAGAGTTCATGCTCA 1698
DB 1450 CAACCGATGTGTGCTCTTCTTATACAGAGCTGATGAAACGAAAGAGTTCATGCTCC 1509
QY 1699 TGA 1701
DB 1510 TGA 1512

RESULT 5
US-10-223-076-5
; Sequence 6, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and

Qy	918	TGACATGAAGTACCTAGCCCAATGCAGCTGATAAGG-----CCAA	956
Db	811	TGATATGAGAGCACTACTGTGTTGGAATGAAAGGGAGAAACATTACCCAACTACTTGAT	870
Qy	957	TCCTGAAGTCTCCCTACTACGTGTGAGAGCTTGGCATATTTCAATGTCGCTCCAC	1016
Db	871	TATGGAGTATCCGTACACTGTGACCTTCAGAGGTTTGGCATCTTCAATGTTGCTCCTAC	930
Qy	1017	ATTGTGTTATCAGCCAAAGTTATCCACGTTCTGCATGTATACGGAAGGTTGGGTGGCTCG	1076
Db	931	ATTATGCTATCAGACAAGCTATCCTCGCACACCTTCAGTTTCTGAAAGGTTGGGTGTTTCG	990
Qy	1077	TCAATTTGGAAACTGTCATATTCACCGGATTCATGGGATTTTATATAGAAACAATATAT	1136
Db	991	TCAACTGTGCAAGCTGATAATATTTACAGAGTTTATGGGATTTTATATAGAAACAATATAT	1050
Qy	1137	AAATCCTATTGTGAGGAACCTCAAGCATCCTTTGAAGGCGATCTTCTATATGCTATTTGA	1196
Db	1051	GAATCCTATTGTACAAAACCTCAACTCATCTTTGAAGGGAAACCTTCTATATGCCATTTGA	1110
Qy	1197	AAGAGTCTTGAAGCTTTCAGTTCCAAATTTATATGTGTGGCTCTGCAATGTTTACTGCTT	1256
Db	1111	GAGAAATCTCAAGCTTCTGCTCCCAATGTATATGTGTGGCTCTGCAATGTTTACTGCTT	1170
Qy	1257	CTTCCACCTTTGGTTAAACATATTTGGCAGAGCTTCTGCTTCGGGGATCGTGAATTTCTA	1316
Db	1171	TTTTCCACCTTTGGTTAAACATATCTGCGAGAGCTTGTTCGATTTGGTGATCGTGAGTTCTA	1230
Qy	1317	CAAGAATTTGGTGAATGCAAAAAGTGTGGGAGATTACTGCGAGAAATGTGGAATATGCTGT	1376
Db	1231	TAAAGTTGGTGGAAATGCGCAAACTGTTGAAGAGTATTTGAGAGTTTGGGAAATATGCTGT	1290
Qy	1377	TCATAAATGGATGGTTGACATATATACTTCCCGTGTCTCGCAGCAGAGATACCAAGAC	1436
Db	1291	GCACAAATGCATGGTTGCGCACACATATTTTCCATGCTTAAAGCGTGGTATACCCAAAGG	1350
Qy	1437	ACTCGCCATATCATTTGCTTTCTTAGTCTCTGCAAGCTTTTCATGAGCTATGCAATGCGAGT	1496
Db	1351	TGCTGCTTCATTAATTTGCATTCTCGGTTTCTGCTGTGTTTCATGAGTTATGCAATGCCGT	1410
Qy	1497	TCCTTGTCGTCTCTTCAAGCTATGGGCTTTCTTGGGATTAATGTTTCAGGTGCTTTGGT	1556
Db	1411	TCCTTGCCACATGTTCAAAGTTGGGCTTTTATAGGAATTAATGTTTCAGGTTCTTTGGT	1470
Qy	1557	CTTCATCACAACTATCTACAGGAAGGTTTGG---CTCAACGGTGGGGAACATGATCTT	1613
Db	1471	CTTGATCAGCTAATTAATCTCCAAAATAATACAGAAACTCAATGGTTGGAAATAATGATTTT	1530
Qy	1614	CTGGTTTCATCTTCTGCAATTTTGGCAACCGATGTGTGCTCTTCTTTATTTACCACGACCT	1673
Db	1531	TUGGTTCATATTTTGTATTTCTTGGTCAACCAATGAGGTAATTTGATCTACCTTGACTT	1590
Qy	1674	GATGAACCGGAAAGGA	1689
Db	1591	GATGAATGAGAAAGGA	1606

RESIST &

```

US-10-424-599-111496
; Sequence 111496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

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Db 1439 TAAAGATTGGTGGATGCCAATACTGTGGAAGATATTGGAGGATGTGGAAATATGCGCTGT 1498
Qy 1377 TCATAAATGGATGGTTCGACATATCTACTCCCGTGTTCGCGACGAGATACCAAGAC 1436
Db 1499 GCACAAATGGATGGTTCGCGACATATATTTCCATGCTTAAGGCGTGGTATACCAAGGG 1558
Qy 1437 ACTCGCCATTATCATTGCTTCCCTAGTCTCTCGAGTCTTTTCATGAGCTATCGATCGAGT 1496
Db 1559 TGGTCTTCATTAAATGGATTCCTGGTTCCTGCTGTGTTCATGAGTATGCAATGCGGT 1618
Qy 1497 TCCCTGTGCTCTCTCAAGGATATCGGCTTTCTTGGGATATGTTTCAAGTGCCTTTGGT 1556
Db 1619 TCCCTGCCACATGTTCAAGTTGGGCTTTTATAGGAATATGTTTCAAGTTCCTTTGGT 1678
Qy 1557 CTTTATCACAAATATCTACAGGAAGGTTGG---CTCAACGGTGGGGAACATGATCTT 1613
Db 1679 CTTGATCACTAAATATCTCCAAATAAATAACAGAACTCAATGGTTGGAATATGATTT 1738
Qy 1614 CTGCTTCATCTCTGCAATTTTCGACACACGATGTGTGCTTCTTTATACACGACCT 1673
Db 1739 TTGGTTCATATTTGTTATCTTGTGTCACCAATGAGGCTATTTGTACTACCATGACTT 1798
Qy 1674 GATCAACCSAAAGGA 1689
Db 1799 GATGAATAGAAAGGA 1814

RESULT 9

US-10-223-076-12
/ Sequence 12, Application US/10223076
/ Publication No. US20030074695A1
/ GENERAL INFORMATION:
/ APPLICANT: Farese, Robert V
/ TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
/ FILE REFERENCE: UCAL-105CIP3
/ CURRENT APPLICATION NUMBER: US/10/223,076
/ CURRENT FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 10/040,315
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 09/339,472
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/107,771
/ PRIOR FILING DATE: 1998-11-09
/ PRIOR APPLICATION NUMBER: PCT/US98/17883
/ PRIOR FILING DATE: 1998-08-28
/ PRIOR APPLICATION NUMBER: 09/103,754
/ PRIOR FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 2099
/ TYPE: DNA
/ ORGANISM: Nicotiana tabacum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (208)...(1806)
US-10-223-076-12

Query Match 36.6%; Score 697; DB 15; Length 2099;
Best Local Similarity 71.5%; Pred. No. 4,6e-194;
Matches 948; Conservative 0; Mismatches 365; Indels 12; Gaps 2;

Qy 376 GATAATAACGGTGGTGGGATATAACGGTGGTGGAGAGCGCGGAGAGGAGGAGGA 435
Db 469 GAGGACGACAGGAATGATAATGTGCGAATGGTGGGAAGCAATCAACGGGAACAACA 528
Qy 436 AACGGGATGCTACGTTTACGATTCACCGTGGTTCAGCTCATTCGAGGCGGAGAG 495
Db 529 ACGACGCCGTTTAAATTTGTTACAGGGGGTGGCACCGACTCACCGGCGGAATCAAGGAG 588

Qy 496 AGTCCACTTAGCTCCGACGCAATCTTCAAAACAGAGCCATGCCGGAATTATTCACCTCTGT 555
Db 589 AGTCTCTCAGCTCCGACGCCATTTTCAACACAGAGTCAAGCAGGCGCTGTTCATCTCTGT 648
Qy 556 GTAGTAGTTCCTTATTTGCTTAAACAGTAGACTCATCATCGAAAACTTATGAAGTATGGT 615
Db 649 GTGGTGGTCTGATTTGCTTTAAACAGCAGGCTGATTCGAGACTTGAAGTATGGC 708
Qy 616 TGGTGTATCAGAACGGATTTCTGCTTTAGTTTCAAGATCGCTCGAGATTGGCGGCTTTTC 675
Db 709 CTTTAAATTAGGCTGGCTTTTGGTTTGTAGCTCGAAGTGGTGGAGATTGGCGGCTTCTA 768
Qy 676 ATGTGTGTATATCCCTTTCCGATCTTCTTGGTGGCTTTTACGGTTGAGAAATGGTA 735
Db 769 ATGTGCTGTCTCAGTCTCCAAATTTTGGCGCTCGCTCTTTTCTTGTGGAGATTGGCA 828
Qy 736 CTTTCAAGAAATACATATCAGAACCTGTGTCTCATCTTTCTTCAATATTATCACCATGACA 795
Db 829 CAGCAGAGGCAATTTGACTGAGGGTGGGTGTACTCTTCACTAATCTATTAACAACAGCT 888
Qy 796 GAGTTTGTATCCAGTTTACGTCAACCTTAAGGTGTGATTCGTCTTTTATCAGGTGTC 855
Db 889 GCCATTGTATCCAGTCTCTGTCAATCTTGGGTGTGATTCGTCTTTTCTGTGTGCTGTC 948
Qy 856 ACTTGTATGCTCTCTCATCTGCAATTTGTGGCTTAAGTTGGTTCTTATGCTCATCTAGC 915
Db 949 ATATTGATGCTGGTGTGCTTGCATTTGTGGAATGAAGCTGGTTCTTACGCACATCAAAAT 1008
Qy 916 TATGACATAAGATCCCTAGCAATGCAGCTCATAGG-----CCAATCCTCAAGTTC 966
Db 1009 CATGATATGAGACAGCTCGCAAGTCTACGACAGGATGAACCTTCAGATGGGATTTTC 1068
Qy 967 TCCTACTAGTTAGCTTGAAGAGCTTGGCAATTTTATGCTGCTGCCACATTTGTTAT 1026
Db 1069 TCTTATCATGTTAGCTTCAAGAGTTTGGCTTACTTTCATGTTTGGCCAACTATGTTAT 1128
Qy 1027 CAGCCAGATTATCAAGTTCTGCAATGTATATCGGAGGGTGGTGGCTCTGTCATTTGCA 1086
Db 1129 CAGCTTAGCTATCCCACTCCCATGCAATTCGAAAGGTTGGGTGGCAGCGCAATTCATC 1188
Qy 1087 AAATGCTCATATTTCAACGGATTCATGGGATTTATATAAGAACAAATATATAATCCTATT 1146
Db 1189 AAGCTGGTAATATTTACAGGATTTGATGGATTTATCATAGAACAGTACATTAACCCAAAT 1248
Qy 1147 GTGAGGAACCTCAAGCATCTTTGAAAGGGGATCTTCTATATGCTATTTGAAGAGTGTG 1206
Db 1249 GTGCAAAACTCACACATCTCTTTGAAAGGAAACCTTTTATATGCCATCGAGAGGATTTG 1308
Qy 1207 AAGCTTTCAAGTTCCAAATTTATATGCTGCTGCAATGTTCTACTGCTTCTCCACCTT 1266
Db 1309 AAGCTTTGGTTCCAAATTTATATGCTGCTGCAATGTTTACTGCTTCTTCTTCTTCTT 1368
Qy 1267 TGGTTAAACATATTTGGCAGAGCTTCTCTGCTTGGGGATCGTGAATCTCAAAAGATTGG 1326
Db 1369 TGGCTAAATATATCTTGGGAATCTATGTTTGGTGTATCTGAGTCTCAAGAGATTGG 1428
Qy 1327 TGGAAATGCAAAAGTGGGAGATTACTGAGAAATGGAATATGCTGTTTCAATAATGG 1386
Db 1429 TGGAAATGCCAAACAAATTTGATGAGTACTGGAGGATGTGGAATATGCTGTTTCAAGTGG 1488
Qy 1387 ATGGTTGACATATATATCTTCCCGTGTCTGCGCAGCAAGATACCAAGACACTCGCCATT 1446
Db 1489 ATGGTTCTGTCACATTTATTTCCCTTGTCTTAAGAAACGGAATTTCAAGGGGGTTCGAATA 1548
Qy 1447 ATCAATGCTTTCTAGTCTCTGAGTCTTTTCAAGCTATGCTATGCTGAGTTCTTGTGCT 1506
Db 1549 CTGATTGCTTTCTTGTATCTGCTGTTTCCAGAGCTGTGTTTGTGTTTCCATGTCGC 1608
Qy 1507 CTCTTCAAGCTATGGGCTTTTCTTGGGATTTATGTTTCAAGTGGCTTTGCTTTCATCACA 1566
Db 1609 CTTTTCAGTGGTGGGCAATTCATGGGAATTTATGTTTCCAGGTTCCTTTGTTGTTTCACTCACA 1668
Qy 1567 AACTATCTACAGGAAGGTT--TGGCTCAACGGTGGGGAACATGATCTTCTGCTTCATC 1623

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1669 AACTTCTTACAAAACAGTTCACAAAGCTCGATGGTGGGCAATATGATGTCTGGTCTTT 1728
1624 TTCTGCATTTTCGCAACACCGATGCTGCTCTTTTATTACACACCTGATGAACCGA 1683
1729 TTCTGCATTTTCGCTCAGCAATGTGTGCTCTGTATTACACCATGTGATGAATAGA 1788
1684 AAGG 1688
1789 AAAAG 1793

RESULT 10
US-10-223-076-14
; Sequence 14, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 63/107,771
; PRIOR FILING DATE: 1998-11-29
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Piralla frutescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1673)
US-10-223-076-14

Query Match 36.3%; Score 692; DB 15; Length 1964;
Best Local Similarity 69.0%; Pred. No. 1.3e-192;
Matches 984; Conservative 0; Mismatches 419; Indels 24; Gaps 2;

QY 285 TTCCGATCATGTGGAGCTCCGCGCAGCGTTAGGATCGGATTTGATTCGGTTGTTAACGA 344
DB 233 TTCCGAAATGTTGCAACGACGCTAATTTGATCGAAATCTCCGCGCGGAGCGGTGA 292
QY 345 TGACGCTCAGGGAACAGCCAAATTTGGCCGAGATATACCGTGGTGGCGATTAATACGG 404
DB 293 ATCCGAGAACGAAACAGCAGATTTATGTTAAGGAGGAGGGCGGAAAGTCAAGCAGAA 352
QY 405 TGGTGGAGAGCGCGGAGAGGAGAGAAACCGGATGCTACGTTTACGTTATCGACC 464
DB 353 TGGAGAACTAGTAATGGAACGGAACCTGATTTATGGCCGTCAAATTCACATTCAGGCC 412
QY 465 GTCGGTTCAGCTCATCGGAGGCGGAGAGAGTCCACTTAGCTCCGAGCGCAATCTTCAA 524
DB 413 GCGCGCGCTGCTCACCGCAAAAATAAGGAGAGTCTCTTAGCTCCGAGCGCATCTTCAA 472
QY 525 ACAGAGCCATGCGGAAATTAACACCTCTGTGTAGTGTCTTAATGCTGTAACAGTAG 584
DB 473 ACAGAGCCATGCGGCGCTTCAAACCTTGTATAGTGTGTGTGTGTGTGTGTGTGTGT 532
QY 585 ACTCATCATCGAAATCTTATCAAGCTGTTGTTGATTCAGAACGGAATTTCTGTGTAG 644
DB 533 ACTAATAATTGAGATTAATGAAGATGGGTGGGTGATCAAAATCAGGATTTTGGTTTAT 592

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QY 645 TTCAAGATCGCTCGAGATTGGCGGCTTTTCATGCTGTGTATATCCCTTTTCTGATCTTTCC 704
DB 593 TTCAACATCGCTTAGGGATTGGCCACTGCTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 652
QY 705 TTGGCTGCTCTTTACCGTTTGAGAAATTTGGTACTTTCAGAAATACATATCAAGAACCTGTGT 764
DB 653 ACTCGCTTCATTTCTTGTGCGAAGTGGTGAACATAAATATATATACCTGAGTGGGTGCG 712
QY 765 CATCTTTCTCATATATTATATACCAAGACAGAGGTTTGTATCCAGTTTACGTCACCT 824
DB 713 AGTCTTTCTTCATGTTTACAATCAACACAGTGGAAATCTTGTTCAGTTTGTGTCTTCT 772
QY 825 AAGGTGTGATTCGCTTTTATCAGGTGTCACTTTGATGCTCTCTCACTGCTGATGTGTG 884
DB 773 TAGGTGTGATTCGCTTGTCTTATCAGGTGTCACTGCTAATGCTCTTGTCTGCTGCTGTATG 832
QY 885 GCTAAAGTTGGTTTCTTATGCTCATACTAGCTATGACATAAGATCCCTAGCCAAATGACG 944
DB 833 GTTGAAGCTCGTTTCTTACGACATACAACTATGATTTGAGAGTACTTTCGAAAATCACT 892
QY 945 TGATAAG-----GCCAATCCGTAAGTCTCTCTACTACCTTAGCTTTAGCTT 983
DB 893 TGATAAGTGGGAAGCTATGTCCAGGTACTGGAACCTCGACTACGCTTATGATGTAAGCTT 952
QY 984 GAAGAGCTTGGCATTTTTCATGCTCGCTCCCATTTGTGTTATCGCCAGTATTCACG 1043
DB 953 TAGAGCTCTGGCATACTTTCATGCTTCTCTCACTGCTGTTTGTGTTTACCGCAAGCTACCTCG 1012
QY 1044 TTCTGCATGTATACGGAAGGTTGGGTGGCTCTCAATTTGCAAACTGCTCATATTTAC 1103
DB 1013 GACAGCTTCATTCGGAAGGTTGGGTGTAAGGCAACTAAATTAAGCTGTAATATTTAC 1072
QY 1104 CGGATTCATGGGATTTATATAGAACAAATATATAATCTTATGTCAGGACTCAAGCA 1163
DB 1073 AGGACTCATGGGATTTATTTATAGAACAGTACATAAAACCCGATCGTTTCAAAATTTCTCA 1132
QY 1164 TCCTTTGAAAGCGATCTCTATATGCTATTGAAAGAGTGTGCAAGCTTCAGTTCGAA 1223
DB 1133 TCCTCTGAAAGGAAACCTTTTATATGCTCAATGAGAGGCTTGAAGCTTCTGTTTCCAA 1192
QY 1224 TTTATATGTGCTCTGCTCTGATGTTTCTACTGCTTTTCCACTTTGGTTTAAACATATTTGC 1283
DB 1193 TTTATATGTGCTCTGCTCTGATGTTTATTTGTTTTCCTACCTCTGCTGCTAAATATATCTGC 1252
QY 1284 AGAGCTTCTGCTTGGGATCGTGAATCTTACAAAGATGCTGGAATGCTGGAATGCTGGAATG 1343
DB 1253 TGAACCTTCTGCTTGGGACCGGTGAGTTTATAAGGATGCTGGAATGCTGGAATGCTGGAATG 1312
QY 1344 GCGAGATTACTGAGAAATGTAATATGCTGTTTCAATAATGATGCTGCTGACATATATA 1403
DB 1313 GGAGGATGCTGAGAAATGTAATATGCTGTTTCAATAATGATGCTGCTGCTGCTGCTGCTGCT 1372
QY 1404 CTTCCGCTGCTTGGCAGCAAGATACCAAGAACCTGCGCATTTATCATTTGCTTTTCTTAGT 1463
DB 1373 CTGCTCATGCTTACAAAATGGAATACCAAGATGAGTGGCAGTTTTCATGCTGCTTCTTGT 1432
QY 1464 CTTCTGAGTCTTTCATGAGCTATGCTGCGCTTCTGCTGCTGCTTCTTCAAGCTATGGGC 1523
DB 1433 GTCTGCGATTTTTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492
QY 1524 TTTTCTTGGGATTTATGTTTTCAGGTGCTTGTGTTTCTTCAACAACATATCTACAGGAAAG 1583
DB 1493 GTTCTCGGATCATGCTTTCAGGTCTCTCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1552
QY 1584 GTT----TGGCTCAACGGTGGGAAACATGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
DB 1553 GTTCAAAAACCTCAATGGTGGCAATATGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1612
QY 1641 ACCGATGTGGGTGCTTCTTATTAACAGACCTGATGAACCGAAG 1687
DB 1613 ACCTATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659

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RESULT 11

US-09-770-444-209/c
 ; Sequence 209, Application US/09770444
 ; Patent No. US20020023280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jom
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Krickler, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurban, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2027 (PARA-016PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,444
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 209
 ; LENGTH: 470
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-444-209

Query Match 24.7%; Score 470; DB 9; Length 470;
 Best Local Similarity 100.0%; Pred. No. 1.5e-127;
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1405	TTCCCGTCTTGGCAGCAAGATACCAAGACACTGCCATATCATTTCTTCTAGTC	1464
DB	470	TTCCCGTCTTGGCAGCAAGATACCAAGACACTGCCATATCATTTCTTCTAGTC	411
QY	1465	TCTGAGCTCTTCAATGAGCTATGATCGAGTTCCTTGTCTCTTCAAGCTATGGCT	1524
DB	410	TCTGAGCTCTTCAATGAGCTATGATCGAGTTCCTTGTCTCTTCAAGCTATGGCT	351
QY	1525	TTTCTTGGGATTATGTTTTCAGGTSCCTTGGTCTTCTATCAACACTATCTACAGGAAG	1584
DB	350	TTTCTTGGGATTATGTTTTCAGGTSCCTTGGTCTTCTATCAACACTATCTACAGGAAG	291
QY	1585	TTTSGCTCAACGGTGGGAAACATCATCTTCTGGTTCTATCTTCTGCAATTTTGGCAACCG	1644
DB	290	TTTSGCTCAACGGTGGGAAACATCATCTTCTGGTTCTATCTTCTGCAATTTTGGCAACCG	231
QY	1645	ATGTGTGTCTTCTTATNATACAGCACTCATGAAACCGAAAGGATCGATGTCTATGAAAC	1704
DB	230	ATGTGTGTCTTCTTATNATACAGCACTCATGAAACCGAAAGGATCGATGTCTATGAAAC	171
QY	1705	AACGTGTCAAAAATGACTTCTTCAACACTATGATGGCTCGTGGATCTCCGTGTATGT	1764
DB	170	AACGTGTCAAAAATGACTTCTTCAACACTATGATGGCTCGTGGATCTCCGTGTATGT	111
QY	1765	TGTGTGGTCTCATGCTAAACGACAAATAGTGTATTAACCATTTGAAGAGAAAGAAA	1824
DB	110	TGTGTGGTCTCATGCTAAACGACAAATAGTGTATTAACCATTTGAAGAGAAAGAAA	51
QY	1825	ATTAGAGTCTTGTATCTGCAAAAATTTTGTGTAGACACGCAAAACCCGT	1874

Db 50 ATTAGAGTCTTGTATCTGCAAAAATTTTGTGTAGACACGCAAAACCCGT 1

RESULT 12

US-10-223-076-17
 ; Sequence 17, Application US/10223076
 ; Publication No. US20030074895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Farese, Robert V
 ; APPLICANT: Cases, Sylvaine
 ; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
 ; FILE REFERENCE: UCAL-105CIP3
 ; CURRENT APPLICATION NUMBER: US/10/223,076
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR FILING DATE: 1998-11-09
 ; PRIOR FILING DATE: 1998-08-28
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 1572
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-10-223-076-17

Query Match 19.9%; Score 379.4; DB 15; Length 1572;
 Best Local Similarity 66.0%; Pred. No. 1.8e-100;
 Matches 576; Conservative 0; Mismatches 276; Indels 21; Gaps 1;

QY	634	TTCTGGTTTATGTTCAAGATGCTGCGAGATGGCGCTTTTCATGTTGTATATACCCCTT	693
DB	1	TTTTGGTTTATGTTCAAGATGCTGCGAGATGGCGCTTTTCATGTTGTATATACCCCTT	60
QY	694	TGATATCTTCTTGGCTGCTTTAAGCTTTCAGAAATGGTACTTCAGAAATACATATCA	753
DB	61	CCGATTTTCCCTTGGCTGCTTTAAGCTTTCAGAAATGGTACTTCAGAAATACATATCA	120
QY	754	GAACTGTGTCTATCTTCTTCAATATATATATATATATATATATATATATATATATAT	813
DB	121	GATCTGTCTATCTATCTTCTTCAATATATATATATATATATATATATATATATATATAT	180
QY	814	TACGTCTACCTTAAGTGTGATCTGCTTTTATATATATATATATATATATATATATATAT	873
DB	181	CTGTGTATCTTAAAGTGTGATCTGCTTTTATATATATATATATATATATATATATATAT	240
QY	874	TGATATGTTGGCTTAAAGTGTGATCTTCTTATATATATATATATATATATATATATATAT	933
DB	241	TGATATGTTGGCTTAAAGTGTGATCTTCTTATATATATATATATATATATATATATATAT	300
QY	934	GCCAAATCAGCTGATTAAGGCAATCTCTGAACTCTCTTACTAGCTTAGCTTCTGAA	986
DB	301	ATCAAGAGGCAAGAGTGTGATAATGAATGACTGACCGGCTGGCATAGATAATTTACAA	360
QY	987	-----GAGCTTGGCATATTTTATGCTCGTCCCATATGCTTGTATATACGCA	1032
DB	361	GCTCCAACTCTTGGGAGTCTTAACATATCTTATGATGCTCGGCTCGGCTTGTATATACGCA	420
QY	1033	AGTTATCTCAGCTTCTGATGATATATACGAAAGTGTGGTGGCTCGTCAATTTGCAAACTG	1092
DB	421	AGTTATCTCAGCACTTATGTTAGAAAGTGTGGTGGCTCGGCTCGGCTTGTATATACGCA	480
QY	1093	GTCAATATCCCGGATTCATGGGATTTTATATAGCAAAATATATAATTCCTATTGTACAG	1152
DB	481	TTGATATTTACTGCTCTCCAAGGATTCATTATTTAGGCAATATATAATTCCTATTGTG	540

QY 1153 AACTCAAGCATCTTTTGAAGCGATCTCTATATGCTATGAAAGAGTGTGAAGCTT 1212
Db 541 AACTCTCAACATCCATGATGGAGGATTAAGTCTGCTAGAGACTGTTTGAAGCTC 600
QY 1213 TCGTTTCCAAATTTATATGTTGGCTCTGATGTTCTACGCTTCTTCCACCTTTGGTTA 1272
Db 601 TCATTACCAAAATGCTACCTGTGGCTTTGATGTTTATGCTTTTCCATCTGTGGTTA 660
QY 1273 AACATATTCGAGAGCTTCTCTGCTTGGGGATCGTGAATTTCTACAAGANTGGTGAAT 1332
Db 661 AACATATTCGCTGAGATCTTCTGATTTGGGATCGGAGAAATTTACAAGACTGGTGAAT 720
QY 1333 GCAAAAAGTCTGGAGATTAAGTGAAGATGCTGAATATGCTCTTTCATAAATGGATGGTT 1392
Db 721 GCAAGAGCAATTTGATGAGTACTGGAGAAATGAAATGCTGCTGCTGATAAATGGATGTT 780
QY 1393 CGACATATATATCTCCGCTGCTTGGGAGCAAGATACCAAGACATCTGGCCATTAAT 1452
Db 781 CGTCATATATATTTCTGCTGATGCGAAATGGTATATCAAGGAAGTGTGCTGTTTTATA 840
QY 1453 GCTTTCCTAGTCTCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485
Db 841 TCGTTCTTTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873

RESULT 13

US-09-770-791-192
; Sequence 192, Application US/09770791;
; Patent No. US200200623141

GENERAL INFORMATION:

; APPLICANT: Goriach, Jom
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(380)
; OTHER INFORMATION: n = A,T,C or G

Query Match 19.5%; Score 371; DB 9; Length 380;
Best Local Similarity 99.5%; Pred. No. 2e-98;
Matches 371; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1046 CTGCATG-ATACGGAAGGTTGGGTGGCTCGTCAATTTGCAAAACCTGGTCATATTCACCG 1105

Db 8 CTGCATGATACGGAAGGTTGGGTGGCTCGTCAATTTGCAAACTGGTCATATTCACCG 67
QY 1106 GATTCTGGGATTTAATAAGAACAAATATAATCCCTATGTGAGAACTCAAAGCATC 1165
Db 68 GATTCTGGGATTTAATAAGAACAAATATAATCCCTATGTGAGAACTCAAAGCATC 127
QY 1166 CTTTGAAGCGGATCTCTATATGCTTATTCGAAAGAGTGTGAAGCTTTCAGTTCAAAT 1225
Db 128 CTTTGAAGCGGATCTCTATATGCTTATTCGAAAGAGTGTGAAGCTTTCAGTTCAAAT 187
QY 1226 TATATGTGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285
Db 188 TATATGTGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
QY 1286 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1345
Db 248 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
QY 1346 GAGATTACTGGGAATCTGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
Db 308 GAGATTACTGGGAATCTGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
QY 1406 TCCGCTGCTTGGG 1418
Db 368 TCCGCTGCTTGGG 380

RESULT 14

US-10-223-076-16

; Sequence 16, Application US/10223076
; Publication No. US20030074695A1

GENERAL INFORMATION:

; APPLICANT: Farese, Robert V
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1181
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 235, 236, 237, 238, 239, 317, 318, 319, 320, 321, 322, 393,
; LOCATION: 394, 395, 396, 397, 398
; OTHER INFORMATION: n = A,T,C or G

US-10-223-076-16

Query Match 19.2%; Score 365.6; DB 15; Length 1181;
Best Local Similarity 67.5%; Pred. No. 1.7e-96;
Matches 500; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 947 ATAAGGCCAATCCTGAACTCCTACTAGCTTACGTTGAGAGCTTGGCATATTTCAATGG 1006
Db 85 ATATGTCGATCCTGAGATATGAAGATCCAACTTTAAAGTCTAGTGTCTTCTATGT 144
QY 1007 TCGTCCCAATGTGTTTATACGCAAGTATCCAGTTCTGCAATGATACCGAAGGTT 1066

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Db 145 TGGCCCAACACACTTGTGGTACCAGCAACTTATCTCTCAAACTACATGTATTAGAAAGGTT 204
Qy 1067 GGGTGGCTCTGCAATTTGGCAAACTGTCATATTCACGGGATTCATGGGATTTTAAATAG 1126
Db 205 GGGTGACCCCACTCATAAAGTGCCTGGNNNNNACAGGCTTGATGGCTTTCATAATG 264
Qy 1127 AACAAATATATAATCCATTTGTTCAGGAACCTCAAAAGCATCTTTGAAAAGGGCATCTCTAT 1186
Db 265 AGCAATATATATACCCCAATTTGTGAGAAATTCCAAACATCCACTGAAAGGGGAANNNGA 324
Qy 1187 ATGCTATGAAAGAGTGTGAAGCTTTTCAGTTCGCAATTTATATGTGTGGCTCTGCATGT 1246
Db 325 ATGCTATGAAAGAGTGTGAAAGCTTTTCAGTTCGCAATTTATATGTGTGGCTTTCATGT 384
Qy 1247 TCTACTGCTCTTCCACCTTTGGTAAACATATTTGGCAGAGCTTCTCTGCTTGGGGATC 1306
Db 385 TCTATTGCGNNNNNCATTTATGGCTGAACTATGAGCTGAACCTCTCTGTTTGGGTGACC 444
Qy 1307 GTCAATTTCTCAAAAGATTGGTGGAAATGCAAAAGCTGTGGGAGATTACTGGGAGATGTGGA 1366
Db 445 GTGAAATCTATAGGACTGTGGAAATGCCAAACTGTTGAAGATCTCGGAGGATGTGGA 504
Qy 1367 ATATGCTGTTCATAAATGGAATGTTGCAATATATATCTTCCCGTGTGTTGGCAGCAAGA 1426
Db 505 ACATGCTGTTCATAAATGGAATGTTGCAATATATATCTTCCCGTGTGTTGGCAGCAAGA 1486
Qy 1427 TACCAAGACACTGCGCATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1486
Db 565 TCTCCAGGGGTGAGCTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 624
Qy 1487 GCATCGAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1546
Db 625 GATGCGGTGCGGTGCGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 684
Qy 1547 TGCCTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1606
Db 685 TACCGTTGGTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 744
Qy 1607 TGAATCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1666
Db 745 ACATGATATTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 804
Qy 1667 ACATGCTGATGAACCGAAG 1687
Db 805 ATGACGTCATGAACGACG 825
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RESULT 15

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US-10-273-438-4
; Sequence 4, Application US/10273438
; Publication No. US2003007257A1
; GENERAL INFORMATION:
; APPLICANT: Faresse, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: USAL-105C1F2
; CURRENT APPLICATION NUMBER: US/10/273,438
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
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; LENGTH: 629

; TYPE: DNA

; ORGANISM: arabidopsis thaliana

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (0)-(0)

; OTHER INFORMATION: Each n residue at position 455, 464, 467, 475, 497, 500, 508,

; OTHER INFORMATION: 514, 519, 536, 543, 544, 576, 583, 584 and 597 can be either a, c,
US-10-273-438-4

Query Match

Best Local Similarity 17.7%; Score 336.4; DB 15; Length 629;

Matches 381; Conservative 0; Mismatches 16; Indels 5; Gaps 3;

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Qy 1047 TGCATGTATACGGAAGGTTGGGTGGCTGTCATTTTGCATAAACTGTGTCATATTCACCGG 1106
Db 1 TGCATGTATACGGAAGGTTGGGTGGCTGTCATTTTGCATAAACTGTGTCATATTCACCGG 60
Qy 1107 ATTCATGGGATTTTATATAGAACATATATAATCCATTTGTGAGAACTCAAGCATCC 1166
Db 61 ATTCATGGGATTTTATATAGAACATATATAATCCATTTGTGAGAACTCAAGCATCC 120
Qy 1167 TTGAAAGGGCATCTTCTATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCAAATTT 1226
Db 121 TTGAAAGGGCATCTTCTATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCAAATTT 180
Qy 1227 ATATGTTGGCTCTGCAATGTTCTACTGCTTCTTCCACCTTTGGTTAAACATATTTGGCAGA 1286
Db 181 ATATGTTGGCTCTGCAATGTTCTACTGCTTCTTCCACCTTTGGTTAAACATATTTGGCAGA 240
Qy 1287 GCTTCTCTGCTTGGGATCTGTAATTTCTACAAAGATTTGGTGAATGCAAAAGTGTGGG 1346
Db 241 GCTTCTCTGCTTGGGATCTGTAATTTCTACAAAGATTTGGTGAATGCAAAAGTGTGGG 300
Qy 1347 AGATTACTT-GGAGAAATGTGGAATATGCTGTTCATATAAAGG-ATGGTTCCGACATATATA 1403
Db 301 AGATTACTTGGAGAAATGTGGAATATGCTGTTCATATAAATGGGATGGGTCCGACATATATA 360
Qy 1404 C--TTCCCGTCTTGGCAGCAAGATACCAAGACATCTCGCC 1443
Db 361 CCTTCCCGTCTTGGCAGCAAGGATTTACCCAAAGACACCCC 402
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Search completed: May 5, 2004, 20:19:39

Job time : 736.533 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	626	12.1	1942	4	US-09-326-203A-1	Sequence 1, Appli
2	143.8	2.7	629	4	US-09-103-754A-3	Sequence 3, Appli
3	135.4	2.6	1446	4	US-09-593-359-1	Sequence 1, Appli
4	135.4	2.6	1512	4	US-09-593-359-3	Sequence 3, Appli
5	100.6	1.9	19124	2	US-08-487-826B-13	Sequence 13, Appl
6	100.2	1.9	10467	4	US-10-204-708-2	Sequence 2, Appli
C 7	98.6	1.9	6669	4	US-10-204-708-5	Sequence 5, Appli
C 8	95.8	1.8	6669	4	US-10-204-708-6	Sequence 6, Appli
C 9	93.8	1.8	6113	4	US-10-204-708-14	Sequence 14, Appl
C 10	93.2	1.8	8961	4	US-10-204-708-80	Sequence 80, Appl
C 11	91.2	1.8	6070	4	US-10-204-708-10	Sequence 10, Appl
C 12	89.6	1.7	6583	4	US-10-204-708-26	Sequence 26, Appl
C 13	87.8	1.7	19124	2	US-08-487-826B-13	Sequence 13, Appl
C 14	87.6	1.7	11049	4	US-10-204-708-23	Sequence 23, Appl
C 15	86.6	1.7	5152	4	US-10-204-708-74	Sequence 74, Appl
C 16	86	1.7	6040	4	US-10-204-708-69	Sequence 69, Appl
C 17	85.8	1.7	6306	4	US-10-204-708-50	Sequence 50, Appl
C 18	85.6	1.6	6317	4	US-10-204-708-11	Sequence 11, Appl
C 19	83.4	1.6	10619	4	US-10-204-708-4	Sequence 4, Appli
C 20	84.6	1.6	5152	4	US-10-204-708-73	Sequence 73, Appl
C 21	83.6	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
C 22	82.4	1.6	6866	4	US-10-204-708-20	Sequence 20, Appl
C 23	82	1.6	6124	4	US-08-213-4-9B-3	Sequence 3, Appli
C 24	81.8	1.6	5666	4	US-10-204-708-23	Sequence 29, Appl
C 25	81.2	1.6	1511	1	US-07-991-867B-8	Sequence 8, Appli
C 26	81.2	1.6	1511	1	US-08-107-755A-8	Sequence 8, Appli
27	81.2	1.6	1511	2	US-08-544-332-8	Sequence 8, Appli

Db 301 ATCTTGATAGGCTTCGTCAGGAAATCGAGATCGGATTCCTTAAAGGACTCTCTCTCT 360
 QY 1885 CTGGTTCGATATAATCTCTCTTCGATGATGTTGGAGCTCCCGCCGAGCGTAGGGATC 1944
 Db 361 CTGGTTCGATATAATCTCTCTTCGATGATGTTGGAGCTCCCGCCGAGCGTAGGGATC 420
 QY 1945 GGATGATTCGGTTCCTTAAAGATGAGCTCAGGGAACAGCCAAATTTGGCCGGAGATAATA 2004
 Db 421 GGATGATTCGGTTCCTTAAAGATGAGCTCAGGGAACAGCCAAATTTGGCCGGAGATAATA 480
 QY 2005 ACGGTGGTGGCGATATAACCGTGTGGAAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAG 2064
 Db 481 ACGGTGGTGGCGATATAACCGTGTGGAAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 2065 ATGCTAGCTTTACGATATCGAGCTCGGTTCAGCTCATCGGAGGCGCGAGAGAGTCCAC 2124
 Db 541 ATGCTAGCTTTACGATATCGAGCTCGGTTCAGCTCATCGGAGGCGCGAGAGAGTCCAC 600
 QY 2125 TTAGCTCGAGCGCAATCTTCAACAG 2150
 Db 601 TTAGCTCGAGCGCAATCTTCAACAG 626

RESULT 2
 US-09-103-754A-3
 ; Sequence 3, Application US/09103754A
 ; Patent No. 6344548
 ; GENERAL INFORMATION:
 ; APPLICANT: Faresse, Robert
 ; APPLICANT: Cases, Sylvaine
 ; APPLICANT: Smith, Steven
 ; APPLICANT: Erickson, Sandra
 ; TITLE OF INVENTION: Diacylglycerol O-acyltran-
 ; TITLE OF INVENTION: sferease
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bozicevic & Reed
 ; STREET: 285 Hamilton Avenue, Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/103,754A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Field, Bret B
 ; REGISTRATION NUMBER: 37,620
 ; REFERENCE/DOCKET NUMBER: 6510-105p
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650 327 3400
 ; TELEFAX: 650 327 3231
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 629 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-09-103-754A-3

Query Match 2.7%; Score 141.8; DB 4; Length 629;
 Best Local Similarity 95.4%; Pred. No. 6.5e-19;

Matches 146; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 3453 TTACATTTTGGCAGTATATAATCTTATGTTCAGGAATCTCAAGCATCTTTTGAAGGGG 3512
 Db 72 TTATAATAGAACAAATATATAATCTTATGTTCAGGAATCTCAAGCATCTTTTGAAGGGG 131
 QY 3513 ATCTTCATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCTCAATTTATATGTGTGGC 3572
 Db 132 ATCTTCATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCTCAATTTATATGTGTGGC 191
 QY 3573 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 3605
 Db 132 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 224

RESULT 3
 US-09-593-359-1
 ; Sequence 1, Application US/09593359
 ; Patent No. 6552250
 ; GENERAL INFORMATION:
 ; APPLICANT: Laroche, Andre J.
 ; APPLICANT: Nykiferuk, Cory L.
 ; APPLICANT: Weselake, Randall J.
 ; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
 ; FILE REFERENCE: 24015US0
 ; CURRENT APPLICATION NUMBER: US/09/593,359
 ; CURRENT FILING DATE: 2000-06-14
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1446
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; OTHER INFORMATION: DGAT2
 ; NAME/KEY: CDS
 ; LOCATION: (82)..(1107)
 US-09-593-359-1

Query Match 2.6%; Score 135.4; DB 4; Length 1446;
 Best Local Similarity 92.8%; Pred. No. 1.4e-17;
 Matches 142; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 3453 TTACATTTTGGCAGTATATAATCTTATGTTCAGGAATCTCAAGCATCTTTTGAAGGGG 3512
 Db 524 TTATAATAGAACAAATATATAATCTTATGTTCAGGAATCTCAAGCATCTTTTGAAGGGG 583
 QY 3513 ATCTTCATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCTCAATTTATATGTGTGGC 3572
 Db 584 ACCTTCATATGCTATTGAAAGAGTGTGAAGCTTTTCAGTTCCTCAATTTATATGTGTGGC 643
 QY 3573 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 3605
 Db 644 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 676

RESULT 4
 US-09-593-359-3
 ; Sequence 3, Application US/09593359
 ; Patent No. 6552250
 ; GENERAL INFORMATION:
 ; APPLICANT: Laroche, Andre J.
 ; APPLICANT: Nykiferuk, Cory L.
 ; APPLICANT: Weselake, Randall J.
 ; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
 ; FILE REFERENCE: 24015US0
 ; CURRENT APPLICATION NUMBER: US/09/593,359
 ; CURRENT FILING DATE: 2000-06-14
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1512
 ; TYPE: DNA

ORGANISM: Brassica rapus
FEATURE:
OTHER INFORMATION: DGAT1
NAME/KEY: CDS
LOCATION: (1)..(1512)
US-09-593-359-3

Query Match 2.6%; Score 135.4; DB 4; Length 1512;
Best Local Similarity 92.8%; Pred. No. 1.5e-17;
Matches 142; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY	3453	TTCAATTTGGGAGTATATAAATCTATGTCAGAACTCAAGCATCCTTTGAAAGCG	3512
DB	929	TTATATAGAGCAATATAAATCCTATGTTAGGAATCAAGCATCCTCTGAAAGGG	988
QY	3513	ATCTTCATATGCTATGAAAGAGTGTGAAGCTTCAGTTCGAATTTATATGTGGC	3572
DB	989	ACCTTCATATGCTATGAAAGAGTGTGAAGCTTCAGTTCGAATTTATATGTGGC	1048
QY	3573	TCGCAATGTTCTACTGCTTCTTCCACCTTTGGT	3605
DB	1049	TCGCAATGTTCTACTGCTTCTTCCACCTTTGGT	1081

RESULT 5

US-08-487-826B-13
Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhauc
APPLICANT: Wellem, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned
REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH21.001C1P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 19124 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-487-826B-13
Query Match 1.9%; Score 100.6; DB 2; Length 19124;

Best Local Similarity 46.2%; Pred. No. 1.8e-10;
Matches 595; Conservative 0; Mismatches 669; Indels 23; Gaps 7;

QY	183	TATACTAAGAAAATTTTGTGTTTGTCTGTTTGAAGCATATGTTTGAATCTTAAA	242
DB	5832	TAAAAATAGATACTAACAATATGCAATACAGAAATAATTTGTATATAAATATA	5891
QY	243	AAAATACTATGTTTAACTTAAATACTAGAGTACACATCAATCTCGAGCATATC	302
DB	5892	TATATAATATATAAAGCAATTAATACTATCAATAGGTAATAGTTTATATATC	5951
QY	303	AAAAACCGTATTCATAGACCGAGTGTGAGAAAT--CAAACTAGAGAGATAATG	360
DB	5952	ATCCCTTTTATATATATTTTGTGTTTGTCTGTTTGTGTTTGTGTTTGTATATA	6011
QY	361	ATATCGTATCTCCAAATCAATCACTTAGAGATATGTAATCTTATGTGTACATAAA	420
DB	6012	ATATAACAAATATAAACAATATCAGTATTTGGAATATAAATAAATTTATCTACATATA	6071
QY	421	TAAATATATATATATATATATATATATCTGTATATATATCTTGTGACAAAAATGGCA	480
DB	6072	TGCAATGA	6130
QY	481	GTCAAAACCATGACTGAATCAAACTATAAGTCTGATTCGAATCAAACTATAAGTCGGATG	540
DB	6131	TTTATATCTATTTTATATCATGCAATTTTATATATTTTATATATATATATATATAT	6186
QY	541	AGTATTAATTTCCAAATGTTTCTATATCTTTACAAACCGGAAATAGATATATATAGATAC	600
DB	6187	ATTATTAATTTTATATAGTAGCATATATGTTTATATATATATATATATATATATAT	6246
QY	601	CAAAAAGTAGATTGTGTATATTTATAGAGATTTGGAAATTTCACTATTCAGGATCT	660
DB	6247	TATAAATATATAGAACATGAACATTTTATTAATAACTCATATTTGAATATATATATAT	6306
QY	661	AZAGTACTTCCCTAAATTAATCAATGCTGTTGAAAAAGCTCAATGAAATGTTGAAATTTG	720
DB	6307	ATGTGTATTTTACTTTA-----TTTTTTTATATATACATAAATAATTTTGAATTTCA	6359
QY	721	GAAAGTTTATTAATTCGGATCTTTTTTTTTTGTGTCGCCCAAAACATTTTATTTTA	780
DB	6360	TAAAAATGCAATGAATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6419
QY	781	TTACAAATATCAACTTATCTTACTACTAATCAATTTCTATCTTTTGTATACCAACAAAT	840
DB	6420	ATATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6479
QY	841	CAATTCATATTTCTATTTTGAATTTTAAAGAAAACACTATTTTACCAAGTTTACAAAATATATA	900
DB	6480	TGATGCTAT	6539
QY	901	AGGAT--TGTGTTTGAAGAAAAGTACAAAGTGAATCTTTTGTGCAAAATATAAATTTG	959
DB	6540	ATAATATATCTACTTTTAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6599
QY	960	ACTTTTAT	1019
DB	6600	ATATAAT	6659
QY	1020	TTCCAAAGTTTATAAATAAAT--ACATTTTCAAGAGCTATTAGTCTCTTTTAAATAATTTCTAA	1078
DB	6660	TGTCCTCTTTTGTATCTCTAATATATATATATATATATATATATATATATATATATAT	6719
QY	1079	AGTGTATCAAGAGCTACCAAT	1138
DB	6720	AAATATACAT	6779
QY	1139	AAATAAATATATGACTTAAATAGTTTGAAGAGCAATGACCTTGTATATATATATATAT	1198
DB	6780	TATATGTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT	6839
QY	1199	TGTACATATAAATAAATTCAGGTTTATAAATAAATAAATAAATAAATAAATAAATAAATAA	1251


```
RESULT 7
US-10-204-708-5/c
; Sequence 5, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: By Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-5

Query Match      1.9%; Score 98.6; DB 4; Length 6669;
Best Local Similarity 47.6%; Pred. No. 3.3e-10;
Matches 324; Conservative 0; Mismatches 354; Indels 3; Gaps 1;

QY      803 TACTACTAAATCAATTCATATCTTGATACCAACAAATCATCTTCATATCTTCTTTTGAATG 862
DB      1767 TACTCTATACACCTTATCATATCTCATATTAATATATATATTTCTTTTAAATAA 1708
QY      863 TTAAAGAAACACATTTTACAGTTACAGTTACAAATATATTAAGGATTTGTGTAGAAAAAA 922
DB      1707 AATATATACAAATTCACACTTAAATAATATATAATCTTAAACCCAAACATATAA 1648
QY      923 AGTACAGTGTGAATCTCTTTTGTCAATATATAAATGACATTTTATATATATATGACTT 982
DB      1647 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1588
QY      983 ATTGAACATGATTACAGAAATTAATCTCTACAAACCTTCCAAAGTTTATATAATAATACAT 1042
DB      1587 TATTAACATTTTCTACACCATCATCTACCATCAATTTCTAAACCTTTTCATCTTCCCA 1528
QY      1043 TTCAAAGACTATAGTCTCTTTAAATATTTCTTAAAGTGATCAAGACTACCAATAT 1102
DB      1527 AATTAAACCTTACTTAATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTA 1468
QY      1103 AATTCAGAAAGTAGAAGTGTGATTTCTTTTGTGCAATATAATTAATGACTTAAATAGT 1162
DB      1467 ACTTCAAAATTTCAAAATTCGCCAAACCTATCATCTATAAAATTTCTTAAATAAAT 1408
QY      1163 TTGGAAGCATTGAATTTGATATATAGATTTGATATGATACATAAAATTTCCAGTTT 1222
DB      1407 TATTACCTTCTATATAAACAACATACATAAATAAATAAATAAATAAATAAATAAATAAATA 1351
QY      1223 ATAAATAATACATTTTCAAAATGCTATATCAGTTCTTTTAAATAATTTTCACTTAAATAA 1282
DB      1350 TTAACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1291
QY      1283 CACTCAATATAGATAAATTTTCTGAATACATACCAATCTGTAACAGAAATTTGACAA 1342
DB      1290 CCCAACACTTCAACTTAAACATCTCAATAATTTAAACAATAAATAAATAAATAAATAAATA 1231
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QY      1343 AAAAAAATAATCAATAGATGAGACAAATAATCAATCAACAGAGATCTTATGC 1402
DB      1230 ATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1171
QY      1403 AAAAAAATAATGATATACATACAAATTAACATATTTGATATTTTAAATAAATAAATAAATA 1462
DB      1170 AACTTATCTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1111
QY      1463 AAAAAATATCCCAACACCGCTT 1483
DB      1110 AAAAAAATAATTAATCTT 1090

RESULT 8
US-10-204-708-6/c
; Sequence 6, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: By Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 6
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-6
```

```
Query Match      1.8%; Score 95.8; DB 4; Length 6669;
Best Local Similarity 46.3%; Pred. No. 1.2e-09;
Matches 636; Conservative 0; Mismatches 692; Indels 45; Gaps 8;

QY      133 TTGACTTAAATAGCTATTGATGTGCAAAAAATGTAATTTAGTTTAAATTTATCTAAAG 192
DB      5013 TTAAACTTTAAAACTATACATTTTAAATTTTAAATTTTATTAATATTTTATCAAAA 4954
QY      193 ABAATTTTCAATTTGCTGTGTTTGAAGCATGTATCTGTTAACTTAAAAAATATGTA 252
DB      4953 AAAAAAACAACACATCTACATAAACAATAAATAAATTAACAAAAATACAACTACTAT 4894
QY      253 TTGTTAATCTTAAAAA-----TGTAGGAGTACACATCAATCTCTCGAGCATAA 300
DB      4893 AACAACTTTAAAAAATACTAACTTACTTACTTAATAAATTTCAAAATCAAACTAA 4834
QY      301 TCAAAACCGTATTCATAGACCGGATGTGAGAAATCAATAGAGATAATGTGATTTTTTAAA 360
DB      4833 CCTAAACCTTAAATAAATAATATATACTAAATAAACCBAATAAATAAATAATACATACAAAAT 4774
QY      361 AT-----ATCGTATCTCAATCAATCAATCACTAGAGATAATGTGATTTCTTT 406
DB      4773 TTTCAAAAAAATCTTCAATTCGTTTAACTATCTACAAATATTAATAAATAATTTAAAAAT 4714
QY      407 ATGTGCTCATATAAATAAATAATATATATATATATATATATATATATATCTTCTATATATGCTTG 466
DB      4713 AAATCAATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 4654
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QY 467 ACAA--AAAATGCCAGTCAAAACCATGCTGAATCAAACTATAAGTCGGATTGATCA 524
Db 4653 AAAA--CTAACTAATACCAAAACCAACAACTTTAATATATCTTAAACCCACACACA 4594
QY 525 AACCTAAGTCGGATGAGTATTAATTTCCATTTATGTTTCTATCTTTTACAAACCGGAAA 584
Db 4593 TTTTATAAAACCCCAACAAACATTAATAAACTACTTAAATATAATAATAATAACAAATA 4534
QY 585 TAGATATATAGATACCAAAAGTAGATTGTTGATATATTTATGAAGATTTGGATTTTC 644
Db 4533 TCGAAATACAAATATCTTAAAAATAAAAAATAATAAAACCAACCACTAAATATAAATTC 4474
QY 645 ATCAATATCAGATCTAAGTAGTCTCCCTAATTAATCAATCATGTCGGTTGAAAAGCTCAAT 704
Db 4473 ATATTCCTTAAATAAATTTAATCTTAATAAAATAAACAACAAACATTAACAAATATTT 4414
QY 705 GAATGTTTGAATTTGGAAAGTTTATTAATTCGGATCTTTTTTTTTTGTGTCGTCCTC 764
Db 4413 CTACTTAATAAATATCTAATATCTAATAAATCCAAAAATAATTTTTTATATATATAT 4354
QY 765 AAACATTTTATTTATACAAATTAATCACTTATCTTACTTACTTAATCAATTCATATC 824
Db 4353 TTAATAAATTA--AAAAAACCCTAATATCTAATAACACTAAAAAATAAACTTAACTTC 4297
QY 825 TTTGATACCAACAAATCATTTTCATATTTCTATTTTGAATGTTTAAAGAAACACTTTTACCA 884
Db 4296 TCTATATTCACAAATTAACAAATTTTAA--AACATCTAACACCCCAAAATTTTACTA 4239
QY 885 GTTCAAAATATTTAAGGATTTGTTTGTAGAAAAAGTACAAAGTTGAAATCTTTTTTGS 944
Db 4238 AAAAAAACAATATATAAAAAACCAATAACAAAAAACTAAAAATTAACGAAAAATACT 4179
QY 945 TCAATATTAATAATGACITTTTAAATATTAATGACITTTTGAACHATGATACAGATTA 1004
Db 4178 AATAAAAAAANA-----ATCATAAATTAATAATAAACCTCATATAAAAAAATATAC 4127
QY 1005 ATCACTACAAAACTTCCAGTTTATATAATAATCACTTCCAAAGACTATTAGTTCTTCT 1064
Db 4126 AGGATATATATCTTTTAAATATAATAATAATAACGCAAAATTAATAAACHTTAAACAT 4067
QY 1065 TAAATATTTCTPAAAGTGATCAAAAGACTA-CCACATATAATTCGAAAAAGTAGAAGTT 1123
Db 4066 AAAAAAATCTTTTATATATATCTCTCTACCCATCTAAATTTTATATAAAATAAAT 4007
QY 1124 GATTTCTTTTGTCAATTAATTAATGACTTAAATAGTTTGGAAAGCCATTTGAACCTGA 1183
Db 4006 TATCTCAACTTTCRAACTAAAAAATAATAATAAAAACTTCAAAAAAATTTTATAACAACA 3947
QY 1184 TTATAGAAATGATAATGTACATAAAAAAATTTCCAGTT--TATATAATATCATTTTTC 1240
Db 3946 ATAAATAAATAAATTTACGAAACAACTATCTTAAAAAACCATATACAAATCCAAAAA 3887
QY 1241 AAATGCTATATCAGTTCTTTTAAATATTTTCACTPAAAAAACAACCTCAAAATATAGATAA 1300
Db 3886 AAATATAACAAACACATTTACGAAATTTAATAACAATAAATAAATAATAATAACAATA 3827
QY 1301 ATTATTTGAAATACATACCACTGTAAACAGAAATTTGACAAAAAATAAAAAAATGAA 1360
Db 3826 ACTTTTAAATAAAAAAACCATAAATAAGTTTATATCCATTAATAATAAAAAAACAATA 3767
QY 1361 ATGAGAATGAAGACAAAAATAAATCACACAGGATCTTATGCAAAAAAATAATATGAAATAC 1420
Db 3766 TCAACAAAAATTAATTTATTAATAAAAAAATAAATAAATAAATAAATAAATTTTCA 3707
QY 1421 ACAATAACCAATTTGATTTTAAAAATAAATAAATAAATAAATAAATAAATAAATCC 1473
Db 3706 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3654
```

RESULT 9

US-10-204-708-14/c

; Sequence 14, Application US/10204708

```
; Patent No. 5677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 14
; LENGTH: 6113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-14
```

```
Query Match 1.8%; Score 93.8; DB 4; Length 6113;
Best Local Similarity 44.9%; Pred. No. 2.8e-09;
Matches 617; Conservative 0; Mismatches 732; Indels 24; Gaps 6;

QY 140 AAAATAGCTATTGATGTCGAAAAAATGATTTTGTAGTTATATAATTTACTAAAGAAAATTT 139
Db 6002 AAAATACATACCTCAACATAAAAAATCTATTACTTCAATATAATAAACAACAAAATTT 5943
QY 200 TTGATTGTCTGTTGTTTAAAGCATATGTTTGTAACTTAAAAAATATGTTTGTAA 259
Db 5942 AAAAATTAGTTTTTAAAAACATCATTTATAATAACAATACAAATATAATATCTTTATA 5883
QY 260 TCTTAAAAATGTAGAGTACACATCAAACTCTCGAGCAATAATCAAAACCGTATTCTCA--T 316
Db 5882 TAAATTTACAAACACATATCATATCTCTATCTATAAAACACTACAAATCAATATAATTT 5823
QY 317 AGACCGATGTGAGATCAAAATAGAGATAATGTGATTTTAAAAATATCGTATCTCCAAA 376
Db 5822 TTAAAAATAACCAAAATAAAAAATCTCTATAAATTAATCAAACTAATTTTAAACATTAAAT 5763
QY 377 TCAATCACTTAGAAGTATGTAATTTCTTTATGTGCTACATAAATAATATATATATA 436
Db 5762 CCCATCTCTTAAATATCTACGTTATCCAAATTTATCTCTTAAATAACAAAATACTTTA 5703
QY 437 TATATATATATATCTTTGTATATATGTCTTGCAAAAAAATTTGCCAGTCAAAAACCATGACT 496
Db 5702 TAAABCTAAATTAATTAATTAATTTTCCGTTTACAAAATA-----AACTAAACCTACT 5650
QY 497 GAATCAAACTATAGTCGGATTTGAATCAAACTATTAAGTCGGATGATTAATTTCCATT 556
Db 5649 ATAAACCAACACTCCACTCTTAAATATATATCTCAATAAAAAATAAAAACTTATTTTCA 5590
QY 557 ATGTTTCTATCTTTTACAAACCGGAAATAGATATTTATAGATACCAAAAAGTAGATTG 616
Db 5589 CGAAACCCATATATAAATTTTCTTACAACTATTTTCAATATCAATCAACCAAACTACAAATA 5530
QY 617 TGTATATTTAGAGATTTTGGAAATTTTCATCTATTCAGGATCTAAAGTACTTCCCTAAT 676
Db 5529 ACTAAATCAAAATACCTTTTAAATAAATAAATAAACAACATATATACATCCATTAAACATA 5470
QY 677 TAAATCATGTGCGTTGAAAAAGCTCAATGAATGTTTGAATTTGGAAAGTTTATTAATTT 736
Db 5469 ATACTAATCAACAATAAAAAA-----AAACAACACTACTAATATATACGTAATAATAAATCTCAAAAA 5413
```


Db 5683 CCTACCTACAAAACCTAABAAACCACTTAAATAAATTAATTTATTAATAATCAATATA 5624
QY 1076 TAAAGTGACCAAGACTACCAATATAATTCAGAAAAAGTAGAAGTGTGATTTCTTTTGG 1135
Db 5623 AAAAAATAAAAAACCTAATTTATACGAATATATATAAAAAAACCAGAAATCCGTTATTA 5564
QY 1136 TCAAAATAAATAATGACTTTAATAATAGTTTGGAAAGCCATGAACTTGAATATAGAAATGA 1195
Db 5563 TAACTATAAAAAAATAAATTTCTAACTATTATTAATAATCAATCAAACTAAAAATAAATAA 5504
QY 1196 TAATGTACATAAAAAAATTCAGAGTTTATAATAAATAATACATTTTCAAACTGTATATCAGT 1255
Db 5503 AATAATTTATGAAAAATATCTATATAAATAAATAAATCAATATTAATAATAAATAAACAATA 5444
QY 1256 TCTTCTTAAATAATTTCTCTATAAAAAACACTCAAAATATAGAAATAAATTTATGAAATAACA 1315
Db 5443 AATACTACGAAAAATATCTTTATTAATAATAAACCATAAAAAATAAATAAATAATTAAT - 5385
QY 1316 TACCAACTGTAAACAGAAATTTGACCAAAAAAATAAATAAATAAATAAATAAATAAATAA 1375
Db 5384 TATAAATAATTAACATTAATAATCCAAAAA-AAAAAATAAATAAATAAATAATCTATTAT 5325
QY 1376 AAAAAATAATCACCAGGAGTCTTTATGCAAAAAAATAAATAAATAAATAAATAAATAAATA 1435
Db 5324 AAAAAATCTAAAAAATAAATTAATTAACAAAAAATAAATAAATAAATAAATAAATAAATAA 1435
QY 1436 GATAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1467
Db 5264 TAACATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5233

RESULT 11

US-10-204-708-10/c
; Sequence 10, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: CLEX, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: By Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PC7/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-10

Query Match 1.8%; Score 91.2; DB 4; Length 6070;
Best Local Similarity 45.7%; Pred. No. 8.9e-09;
Matches 497; Conservative 0; Mismatches 563; Indels 28; Gaps 4;
QY 393 TAAATGTAATCTTTATGTGCTACATCAATATATATATATATATATATATATATATATCTT 452
Db 2688 TAAATATATCTTCCACATCA 2629
QY 453 GTATATATGTCTTGACAAAAAATTCAGTCAAAAAACCATGACTGAATCAAACTATAGT 512

Db 2628 TCTATTATAAATCAATCTAAATTTTTCCTTTTAACTATTATAATAAATAAATAAATAAAT 2569
QY 513 CGGATTCGAATCAAACTATAAGTCGGATGAGTATTAAATTTCCATTAATGTTCTTACTACTTTA 572
Db 2568 CTTTATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2509
QY 573 CAAACCGGAAAAATAGATATTTATAGATACCAAAAAAGTAGATTTGTGTATATATTATAGAAG 632
Db 2508 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2449
QY 633 ATTTGCAATTTCAATCAATATACAGATCTAAAGTACTTTCCCTAAATTAATCATGTCGGTTG 692
Db 2448 AITTTTCACTCCCATCAACACTATATAAATAAATCCCATTTCTACATCTTTTACAACATAAAA 2389
QY 693 AAAAACTCAATGAATGTTTGGAAATTTGGAAGTTTATTAAATTCGGATCTTTTCTTTTCTT 752
Db 2388 AATTAATCAATCTTTTCAATTTCAACTATCTCTAATAATATTTAATAATATCATATTTTAAT 2329
QY 753 GTTTGTGTCGCCAAACATTTTTTATTATTTTATTAACAATAATCAACTTATCTTACTACTAAA 812
Db 2328 TTCAATTTTACCATAAAAAATTTTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATA 2269
QY 813 TCATTTCATATCTTTGATACCAACAAATCATTTTCATTTCTATTTTGTATGTTTAAAGAAA 872
Db 2268 AAAAACTCTTTCTCGTATTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2209
QY 873 CACTATTTACCAGTTTACAAAAATATTATTA- - - - -GGATTGCTGTTTAGAAAAA 921
Db 2208 CATTAATGCAATTAACCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2149
QY 922 AAGTACAGTTGCAATCTTTTGTCAAAATATAAAATTTGACTTTTAAATATATAATTTGACT 981
Db 2148 ATAAACAAAAATAATATATACATATATAATAAATAATTTTAACTTCAAAAAAATAAATAA 2089
QY 982 TATTCGAATGATTACAGAAATTAATCATCTACAAAACTTCCAGTTTATTAATAAATAACA 1041
Db 2086 TTCTAATACATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2029
QY 1042 TTTCAAAGACTATTAGTTCTTCTTAAATAATTTCTTAAAGTGTATCAAGACTACCAACATA 1101
Db 2028 AATCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1969
QY 1102 TAAATTCAGAAAAAGTAGAATTTGATTTCTTTTGTCAAAATAAATAAATTTGACTTAAATAG 1161
Db 1968 CAAAAAATAACAAATATCGACTATAAAAAAATTA- - - - -AAAAAAGCAATAAOCGAAAAATTTACTA 1911
QY 1162 TTTGCAAAAGCCATTCGAATTTGATTTAGATTAAGTATGATGATCAATAAAAAATTTCCAGTT 1221
Db 1910 TATAAACAACAATAATTTCTTATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1851
QY 1222 TATATAAATAATACATTTTCAAAATGCTATATCAGTTCTTCTTAAATAATTTTCACTAAAAAA 1281
Db 1850 TAAATTTCAACAATAATATAAATAATCTTAATA- - - - -CCATAAATATATACACTTAAAA 1798
QY 1282 ACATCTCAATATAGATAAATAATTTATGATTAACATACCAACTGTAAAAACAGATTTTGACA 1341
Db 1797 ATAATAAATTTTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1738
QY 1342 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1401
Db 1737 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1685
QY 1402 CAAAAAATAATATGAATACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1461
Db 1684 -AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1626
QY 1462 GAAAAAATA 1469
Db 1625 AAAAAAATA 1618

RESULT 12

RESULT 13
 US-08-487-826B-13/c
 Sequence 13, Application US/08487826B
 Patent No. 5993827
 GENERAL INFORMATION:
 APPLICANT: Sim, Kim L.
 APPLICANT: Chitnis, Chetan
 APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 City: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92560
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19124 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-487-826B-13

Query Match 1.7%; Score 87.8; DB 2; Length 19124;

Best Local Similarity 44.8%; Pred. No. 5.3e-08;

Matches 577; Conservative 0; Mismatches 682; Indels 30; Gaps 5;

QY 211 GTTGTTCAGCATGCTATGTTTAAACCTTAAACCAATATGCTGTTTAACTTAAACATG 270
 DB 7178 GTAGAAATAGAAATATTAACACTTTTGTGAATGTATATCATATATATATATATAT 7119
 QY 271 TAGAGATACACATCAATATCTGAGCATATATCAAAACCGTATTCATAGACCGATGTGAGA 330
 DB 7118 TATTACAAATATATATATATGTTATATATATATATATATATATATATATATATATAT 7059
 QY 331 ATCAATAGAGATATATGCTGATTTTAAATATATCGTATCTCCAAATCAATCACTTAGAA 390
 DB 7058 ATATATATCAATATATATATGTTTAAACCAATATATATATATATATATATATATAT 7000
 QY 391 GATCAATGTAATCTTATGCTACATAAATAATATATATATATATATATATATATATAT 450
 DB 6999 AATATTAGTTTATATATTTTAAACCAATATATATATATATATATATATATATATAT 6940
 QY 451 TTGTATATATCTCTCGACAAACCAATTCGAGTCAAAACCAATGCTGATCAACTATAA 510
 DB 6939 ATTAAATATCTTAAACCAAAACCAATATATATATATATATATATATATATATATAT 6880
 QY 511 GTCGGATGTAATCAACTATATAGTCGATGAGTATTAATTTCCATATATGTTCTATCTT 570
 DB 6879 TATTATCTATTTAAT 6820
 QY 571 TACAAACCGAAATACATATATATAGTACCAAAACCAATGATGTTGATATATATATAGA 630
 DB 6819 TATATATGAAAT 6760
 QY 631 AGATTTGCAATTTATCAT 690
 DB 6759 GTTTATATATTTAATTTAATATATATATATATATATATATATATATATATATATAT 6700
 QY 691 TGAACCAAGCTCAATGATGTTTGAATTTGCAATTTGCAATTTGCAATTTGCAATTTT 750
 DB 6699 TATTAT 6640
 QY 751 TTGTTTCTGTCGCAACATTTTATTTTATATATATATATATATATATATATATATATAT 810
 DB 6639 CTATCTAT 6580
 QY 811 -----AATCATTTATATCTTTTATATATATATATATATATATATATATATATAT 846
 DB 6579 TTCTTTGATTTGTTAT 6520
 QY 847 ATATCTATTTTGTATTTAAGAAACATATTTTACCAATTTTACCAATTTTACCAATTTT 906
 DB 6519 AT 6460
 QY 907 GTTGTTCGAAACCAAT 966
 DB 6459 TAACAGCAAAAT 6400
 QY 967 AAT 1026
 DB 6399 TTGTTTGTGTTATTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTT 6340

QY 1027 TTTTAT 1083
 DB 6339 TATAAT 6280
 QY 1084 ATCAAGACTTACCAT 1143
 DB 6279 ATTAAT 6220
 QY 1144 ATATTCAGCTTAAAT 1203
 DB 6219 ATACAT 6160
 QY 1204 ATAAAT 1262
 DB 6159 AAAAT 6100
 QY 1263 AAAAT 1322
 DB 6099 TAT 6040
 QY 1323 TGTAAAT 1381
 DB 6039 TACTGAT 5980
 QY 1382 AATCAACAGAGGATCTTATGCAAAACCAATATATATATATATATATATATATATATAT 1441
 DB 5979 ACAAAT 5920
 QY 1442 TTTAAAT 1470
 DB 5919 TTTTATGTTCTTAT 5891

RESULT 14

US-10-204-708-23/c

Sequence 23, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

PRIOR FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/EP01/03971

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 23

LENGTH: 11049

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-23

Query Match

Best Local Similarity 1.7%; Score 87.6; DB 4; Length 11049;

Matches 498; Conservative 0; Mismatches 579; Indels 23; Gaps 4;

QY 399 AATCTTTATGCTGCTACATAAATATATATATATATATATATATATATATATATATATAT 458
 DB 8426 ATTTCTTTTAAAAAAT 8367

	QY	459	ATGTCCTGTGCAGAAAAAATTGCCAGTCCAAAACCATGACTGAATCAAACTATAAGTCGGATT	518
	Dd	8366	ATTTTCTATAAAATTAATATCAAAAAACAATAATATTAATAATAAAAAACAATAATTAATAAT	8307
	QY	519	GAA-----TCAAACCTATAAGTCGGATGAGTATTAATTTTCCATTTATGTTTTCTATCTTTAC	573
	Dd	8306	AAAAAAATTTAAAAAAACCTTCATATATTAATAAAAAAATAAAAAACGTCATTAATAATA	8247
	QY	574	AAACCGGAAATATAGATATTTATAGATACCAAAAAAGTAGATTTGTGTATATTTATTAAGA	633
	Dd	8246	AAAAAACTAAATATAATTTTAANTACCATAAATCACCATTACCTTTAATAAAAAAATTTTC	8187
	QY	634	TTTGGAATTTCACTCAATTAACAGATCTAAAGTACTTCCTTAATTAATCATGTCGGTGA	693
	Dd	8186	AAACCCAACCTTAATACTCACACTATAATCCCAACACTTTAAAAAACCAAAACGAATAA	8127
	QY	694	AAAGAGCTCAATGAATGTTTGAAATTTTGGAAAGTTTATTAATTCGAATCTTTTTTTTTTG	753
	Dd	8126	ATCACCTAAATTCGTAACCAACCTAAACCAACATAATAAAACCCATCTCTACTAAAAATA	8067
	QY	754	TTTGTGTCGCCAAACATTTTATTTTATTAACAATTAATTAATCTTCTTACTACTAAATC	813
	Dd	8066	CAAAAAATTAACCAAAACGTAATAATACATACCTATAATCCCACTACTTCGAAAAACCTAAAH	8007
	QY	814	CATTTCATACCTTTTGATACCAACAAATCAATTCATATTCATTTTCATGTTTAAAGAAAC	873
	Dd	8006	CACGAAATTCGCTTAACCCCAAAACCAAAATTAACAATAACTTAATCAGACCCGAA	7947
	QY	874	ACTATTTCACAGTTACAAAATATTAAGAATGTTGTTTGTAGAAAAAAAAGTACAAGTTG	933
	Dd	7946	ACTCCCAACCTAAACACAAAAATATAAACTCTATCTCGAAAAATAAAAAAATTCATAAA	7887
	QY	934	AATTCCTTTTGTGCAATATAAAAATTCGCTTTTAAATATATAATTAATGACTTATTCGAA	993
	Dd	7886	AACGATTAACCAAAACCAAACTATAATAATTAATAATTAATTAATTAATAAAAAATAA	7827
	QY	994	TTCAGAAATTAATCATC-TACAAAACTTTCCEAAGTTTNTAATAAATACATTTTCAAAAGCT	1052
	Dd	7826	ATAAAAAATATAAAACCCACAAAAAATAAACCTTCCTTTAAAAAACTTACCTCTCAACAA	7767
	QY	1053	ATTAGTCTTCTTAAATAATTTCTAAAGTGTCAAGACTACCAATATAATTCAGAAA	1112
	Dd	7766	AAAAACAACCTACAATAATAAATAATATAATAACTTATTAATAATTAATAAAAAAACTAAAC	7707
	QY	1113	AAGTAGAAGTTGATTTCTTTTGTGCAATATAAATTAATGACTTAAAAATAGTTTCGAAAGCC	1172
	Dd	7706	AAAAAAATTAACACGTAATAACTTAATAAAAAAACHAAAAATAACCCAAAAAATAT	7647
	QY	1173	ATTGAACTTGATATAGAATTGATATGTTACATAAAAAAATTCOAAGTTTATTAATTAATA	1232
	Dd	7646	ACCFAAAAAACACAAAAATAAAAAATCGCAACAAAAATAAACAAAAACAACAACA	7587
	QY	1233	CATTTTCAAAATGCTA-----TATCAGTTCTTCTTAAAAATATTTCCACTA	1276
	Dd	7586	TCHTTCTCGAACTCTAACAAAAAATAATTCCTTAATAATCTAAATTTTCAAAATAAAAA	7527
	QY	1277	AAAAAACACTCAATAATAGAAATAAATTTATTTGAATTAACACCACTGTAACCAAGAT	1336
	Dd	7526	AAAAAAACTAAATAAATTAACAACAAATATCCCCAATAACCAACAAATTA-ACAAAT	7468
	QY	1337	TGACAAAAAATAAAAAATTAATCGAGATGNAGACAAATAATTAATCACCAGAGATC	1396
	Dd	7467	CCTTAATCAAAAAACAAANTTAAACCTTAACCTAAAAACTAAAAATCTAAAAATTAATATC	7408
	QY	1397	TTATGCAAAAAATAATCATTAATGATACAAATAAACCATATTCATATTTTAAAAATAAATAA	1456
	Dd	7407	CTATACAAAAAATAAAAAATTAACAAAAAACAACACTTAATTAATTAATAAAAAACCT	7348
	QY	1457	AAACAGAAAAAATATCCCAAC	1476
	Dd	7347	ACCTAAAAAATCTCCCACAC	7328

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RESULT 15
US-10-204-708-74/c
; Sequence 74, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPERROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 74
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-74

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Query Match	1.7%	Score	86.6	DB	4	Length	5152
Best Local Similarity	43.4%	Pred.	No.	6.7e-08			
Matches	659	Conservative	0	Mismatches	839	Indels	19
Gaps							
QY	160	AAAAATGATATTTTAGTTGTTATATAATTTATAGTAAAGAAATTTTTCGATTTTGTCTGTCGTGTTAA	219				
Db	2538	AAACAAATTTTTCGGATATACCTGCACTATCCAAACCTATACCTACTTTTATTTCTCC	2479				
QY	220	GCATATGTAATTTGTTTAAACITTTAAAAAATATGTATTTGTATCTTAAAAATGTAGGAGTAC	279				
Db	2478	TATCTTTCCTTAAATTTATAACCTTATTTTATACCTATCTCCATTAAATATAAATTC	2419				
QY	280	ACATCAATCTCGAGCATTAATCAAAACCGTATTCATAGCCGATGTGAGAACTAAATAG	339				
Db	2418	ATATTAACAAAAACATTTACTCTTTAAACAATTTCTACAAACATATAAATATATAT	2359				
QY	340	AGGATATGTGATTTTAAAAATCTCGTATCTCCAATCAATCACTTTAGAGATTAATGTA	399				
Db	2358	TATCAACA-----AAATTCAAAAATTTATATCTCTAAAAAAACCTAATATATAAATAAT	2303				
QY	400	ATTCTTTATGTGTCATATAAATAAATATATATATATATATATATATATATATATATAT	459				
Db	2302	CCTAACTCTCTAAATTTTAAATTTTACTTTTAAATAATAAATTTATATCTTATACTTC	2243				
QY	460	TGCTTTGACAAAAAATGCGAGTCAAAAACCATGACGATCAACTAATAGTCGGATTG	519				
Db	2242	CAAAAAATAAAAAAATACCTAAATATAATATCTTAAACAATACTTTTAAAAATATACCT	2183				
QY	520	AATCAACTATAAGTCGGATGAGTATTAATTTCCATTTATGTTCTTACTTTTCAAAACCG	579				
Db	2182	ATTCATTTTCAATACCTTAAATACCAATTCACAATCTTTTAACTACTTAACTACAAAA	2123				
QY	580	GAATAATAGATATTATAGATACCAAAAAAGTAGATTTCTGTATATTTATAGAGATTTGGA	639				
Db	2122	CACCTTTTACCATATAAATTTTATATATATATATATATATTAATAAACTATTTTACTTTATA	2063				
QY	640	ATTTCACTATTCAGGATCTAAAGTACTTCCCTTAATTAATTAATGATGCTGGTTGAAAAAGC	699				
Db	2062	TATATTAACTAAATAATTTTTTAAATACCTACTATAAATTTTAAATAATATACCTAACCTAC	2003				


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; LENGTH: 470
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-209

Query Match
Best Local Similarity 5.3%; Score 277.4; DB 9; Length 470;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4675 GGTGGGAAACATGATCTTCTGGTTCATCTCTGCAATTTTCGGACACCGATGCTGCT 220
Db 279 GGTGGGAAACATGATCTTCTGGTTCATCTCTGCAATTTTCGGACACCGATGCTGCT 220
QY 4735 TCTTTATTACACGACCTCATGACCGGAAGGATCGATGCTCATGAAACACCTGTTCCAA 4794
Db 219 TCTTTATTACACGACCTCATGACCGGAAGGATCGATGCTCATGAAACACCTGTTCCAA 160
QY 4795 AAATGACTTTCCTCAACATCATGCGCTCGTTGGATCCTCGTTGATGTTGTTGGTGGTTC 4854
Db 159 AAATGACTTTCCTCAACATCATGCGCTCGTTGGATCCTCGTTGATGTTGTTGGTGGTTC 100
QY 4855 TCATGCTAAACGACAAATAGTGTGTTATACCATTTGAAGAGAAAAAGAAATTAGAGTTGT 4914
Db 99 TGATGCTAAACGACAAATAGTGTGTTATACCATTTGAAGAGAAAAAGAAATTAGAGTTGT 40
QY 4915 TTTATCTGCAAAATTTTGGTAGACACGCGAACCCGT 4953
Db 39 TTTATCTGCAAAATTTTGGTAGACACGCGAACCCGT 1

RESULT 4
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: D-agnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/-208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-2-20
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match
Best Local Similarity 3.1%; Score 161.6; DB 15; Length 3673778;
Matches 689; Conservative 0; Mismatches 769; Indels 6; Gaps 6;

QY 35 TATTATTTCAAAGTTTAATATCTCTTTGTATACATCTCAATCTTCACATGATGAT 94
Db 1714596 TATTATCAATAAATATATATATAAATAATATATACATAAATAATATATAAATAATATATA 1714537
QY 95 GTGTGAAACCCCGACAGATTTTACTACATATAGGGGAGTGGTACTTAAATAGCTATTGAT 154
Db 1714536 TAAAAATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATAT 1714477
QY 155 GTCGAAAAATATGATTTTATGTTATTAATATA-CTAAGAAAAATTTTGTGTTGCTGT 213
Db 1714476 ATAAAAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATA 1714417
QY 214 GTTTAAGCATATGATTTGTTAACTTAAATAATATGTTGTTAACTTTTAAATATGATAG 273
Db 1714416 AAATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1714357
QY 274 GAGTACATCAATCTCGAGCATTAATCAAAACCGTATTTCATAGCCGATGTGAGATC 333
Db 1714357 GAGTACATCAATCTCGAGCATTAATCAAAACCGTATTTCATAGCCGATGTGAGATC 333

Db 1714356 ATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1714298
QY 334 AAATAGAGAGATAATGTCATTTTAAATAATCTGATCTCCAAATCAATCACTTGAAGAT 393
Db 1714297 AATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1714238
QY 394 AATGTAATCTTTATGTCCTACATAAATAATATATATATATATATATATATATATATATAT 452
Db 1714237 ATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAA 1714178
QY 453 GTATATATGCTCTGACAAAAAATTCAGTCGCAAAACCAACGACGATCAAACTATAAGT 512
Db 1714177 ATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1714118
QY 513 CGGATTTGAATCAAACTATATAGTCGGATGAGTATTAATCTCCATTTCTATACCTTTA 572
Db 1714117 TATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1714058
QY 573 CAACCGGAAAAATAGATATTTATAGATACCAAAAAAGTAGAT-TGTGTATATATATATAGAA 631
Db 1714057 ATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713998
QY 632 GATTTTGGAAATTTTCATCATTTATCAGGATCTAAAGTACTTCCCTTAATTAATCACTGCT 691
Db 1713997 TATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713938
QY 692 GAAAAAGCTCAATGAATGTTTGAATTTGAAAAAGTTTATTAATTTCCGATCTTTTTTTTT 751
Db 1713937 ATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713878
QY 752 TGTTCCTGCTCCAAACATTTTATTTTATACAAATAATCAACTTATCTTACTACTAA 811
Db 1713877 AAATATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATA 1713818
QY 812 ATCAATTTTCATCTTTGATACCAACCAATCATTTTCATATTTCTATTTTGTGTTTAAAGAA 871
Db 1713817 TATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAA 1713758
QY 872 ACACATTTTACCAGTTTACAAAAATATTTAAGGATTTGTTTGAAGAAAAAAGTCAAGT 931
Db 1713757 TATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713698
QY 932 TCAATTTCTTTTGTCAATATATAAATTTGACTTTTAAATATATAATTTGACTTTTGAACAT 991
Db 1713697 AATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713638
QY 992 GATTACAGAAATTAATCATCTCAAAACCTTTCCAAAGTTTATATAAATAATACATTTTCAAGAC 1051
Db 1713637 ATAAAAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATA 1713579
QY 1052 TATTAGTTCTCTTAAAAATATTTCTAAAAAGTGCATCAAGACTACCAATATATATATTCAGAA 1111
Db 1713578 TATAAAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713519
QY 1112 AAAGTAGAAGTTGATTTCTTTTGTGCAATAAATAATTAATGCACTTAAATAGTTTGGAAAGC 1171
Db 1713518 ATATAAAAATATATATAAATAATATATAAATAATATATAAATAATATATAAATAAT 1713459
QY 1172 CATTCGAACTTGATTTAGAAATTTGATGTAATGTACATAAAAAAATTTCCAAAGTTTATATAA 1231
Db 1713458 TATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATA 1713399
QY 1232 ACATTTTCAAATGCTATAT-CAGTTCTTCTTAAAAATATTTTCACTAAAAAACAACCTCAA 1290
Db 1713398 ATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATA 1713339
QY 1291 TATAGAAATTAATTTTGAATTAACATCCACTGTGTAACAGAAATTTGCAAAAAAATAA 1350
Db 1713338 TATAAACAATATATAAATAATATATAAATAATATATAAATAATATATAAATAATATATAAATA 1713279
QY 1351 AAAAAATCAAAATGAAGATGAAGACAAAAAATAATCAACGAGGATCTTTATGCAAAAAAAT 1410
Db 1713279 AAAAAATCAAAATGAAGATGAAGACAAAAAATAATCAACGAGGATCTTTATGCAAAAAAAT 1410
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[illegible][illegible]

; Sequence 192, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jom
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Naja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(380)
; OTHER INFORMATION: n = A,T,C or G

US-09-770-791-192

Query Match 2.7%; Score 141.8; DB 9; Length 380;
Best Local Similarity 95.4%; Pred. No. 1.4e-14;
Matches 146; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3453 TTACATTTGGCAGTATATAATCCTATTGTCAGGAAGCTCAAGCATCCTTTGAAAGCG 3512
DB 80 TTATAAGAACATATATAATCCTATTGTCAGGAAGCTCAAGCATCCTTTGAAAGCG 139
QY 3513 ATCTTCTATATGCTATTGAAAGAGTGTGAAAGCTTTCAGTTCCAAATTTATATGTGTGGC 3572
DB 140 ATCTTCTATATGCTATTGAAAGAGTGTGAAAGCTTTCAGTTCCAAATTTATATGTGTGGC 199
QY 3573 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 3605
DB 200 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 232

RESULT 7
US-10-273-438-4
; Sequence 4, Application US/10273438
; Publication No. US20030072757A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/273,438
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/10/040,315
; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Each n residue at position 455, 464, 467, 475, 497, 500, 508,
; OTHER INFORMATION: 514, 519, 536, 543, 544, 576, 583, 584 and 597 can be either a, c,
US-10-273-438-4

Query Match 2.7%; Score 141.8; DB 15; Length 629;
Best Local Similarity 95.4%; Pred. No. 1.7e-14;
Matches 146; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3453 TTACATTTGGCAGTATATAATCCTATTGTCAGGAAGCTCAAGCATCCTTTGAAAGCG 3512
DB 72 TTATAAGAACATATATAATCCTATTGTCAGGAAGCTCAAGCATCCTTTGAAAGCG 131
QY 3513 ATCTTCTATATGCTATTGAAAGAGTGTGAAAGCTTTCAGTTCCAAATTTATATGTGTGGC 3572
DB 132 ATCTTCTATATGCTATTGAAAGAGTGTGAAAGCTTTCAGTTCCAAATTTATATGTGTGGC 191
QY 3573 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 3605
DB 192 TCTGCATGTTCTACTGCTTCTTCCACCTTTGGT 224

RESULT 8
US-10-223-076-1
; Sequence 1, Application US/10223076
; Publication No. US:0030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 455, 464, 467, 475, 497, 500, 508, 514, 519, 536, 543, 544,
; LOCATION: 576, 583, 584, 597
; OTHER INFORMATION: n = A,T,C or G
US-10-223-076-1

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Query Match          2.7%  Score 141.8;  DB 15;  Length 629;
Best Local Similarity 95.4%;  Pred. No. 1.7e-14;
Matches 146;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

QY 3453 TTACATTTGGCAGTATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 3512
DB 72 TTATAATAGAACAAATATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 131

QY 3513 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 3572
DB 132 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 191

QY 3573 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 3605
DB 192 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 224

RESULT 9
US-10-040-315A-4
; Sequence 4, Application US/10040315A
; Publication No. US20030167483A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/040,315A
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 629
; TYPE: DNA
; ORGANISM: arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Each n residue at position 455, 464, 475, 500, 508, 514
US-10-040-315A-4

Query Match          2.7%  Score 141.8;  DB 15;  Length 629;
Best Local Similarity 95.4%;  Pred. No. 1.7e-14;
Matches 146;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

QY 3453 TTACATTTGGCAGTATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 3512
DB 72 TTATAATAGAACAAATATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 131

QY 3513 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 3572
DB 132 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 191

QY 3573 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 3605
DB 192 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 224

RESULT 10
US/10/659
; Sequence 4, Application US/10659800
; Publication No. US20040078836A1
; GENERAL INFORMATION:

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; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2CON2
; CURRENT APPLICATION NUMBER: US/10/659,800
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 629
; TYPE: DNA
; ORGANISM: arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Each n residue at position 455, 464, 475, 497, 500, 508, 514
US/10/659,800-4

Query Match          2.7%  Score 141.8;  DB 17;  Length 629;
Best Local Similarity 95.4%;  Pred. No. 1.7e-14;
Matches 146;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

QY 3453 TTACA-TTTGGCAGTATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 3512
DB 72 TTATAATAGAACAAATATATAAATCCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 131

QY 3513 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 3572
DB 132 ATCTTCTATATGCTATGAAGAGTGTGAAGCTTTCAGTTCCAAATTTATATGTGTGGC 191

QY 3573 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 3605
DB 192 TCTGCATGTTCTACTGCTTCTCCACCTTTGGT 224

RESULT 11
US-10-223-076-6
; Sequence 6, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; FILE REFERENCE: UCAL-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1446

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; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1107)
US-10-223-076-6

Query Match      2.6%; Score 135.4; DB 15; Length 1446;
Best Local Similarity 92.8%; Pred. No. 3.2e-13;
Matches 142; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3453 TTACATTTTGGCAGTATATAATCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 3512
Db 524 TTATAATAGAGCATATATAATCTATTGTTAGGAACCTCAAGCATCCTTTGAAAGGCG 583
QY 3513 ATCTTCTATATGCTATTGAAGAGTGTTGAAGCTTCAGTTCCAAATTTATATGTGTGGC 3572
Db 584 ACCTTCTATATGCTATTGAAGAGTGTTGAAGCTTCAGTTCCAAATTTATATGTGTGGC 643
QY 3573 TCTGCATGTTCTACTGCTCTCTTCCACCTTTGGT 3605
Db 644 TCTGCATGTTCTACTGCTCTCTTCCACCTTTGGT 676

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RESULT 12
US-10-223-076-8
; Sequence 8, Application US/10223076
; Publication No. US20030074695A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V
; APPLICANT: Cases, Sylvaine
; TITLE OF INVENTION: Plant Diacylglycerol O-transferase and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: UCAJ-105CIP3
; CURRENT APPLICATION NUMBER: US/10/223,076
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1512)
US-10-223-076-8

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Query Match      2.6%; Score 135.4; DB 15; Length 1512;
Best Local Similarity 92.8%; Pred. No. 3.3e-13;
Matches 142; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3453 TTACATTTTGGCAGTATATAATCTATTGTCAGGAACCTCAAGCATCCTTTGAAAGGCG 3512
Db 929 TTATAATAGAGCATATATAATCTATTGTTAGGAACCTCAAGCATCCTTTGAAAGGCG 988
QY 3513 ATCTTCTATATGCTATTGAAGAGTGTTGAAGCTTCAGTTCCAAATTTATATGTGTGGC 3572
Db 989 ACCTTCTATATGCTATTGAAGAGTGTTGAAGCTTCAGTTCCAAATTTATATGTGTGGC 1048
QY 3573 TCTGCATGTTCTACTGCTCTCTTCCACCTTTGGT 3605
Db 1049 TCTGCATGTTCTACTGCTCTCTTCCACCTTTGGT 1081

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RESULT 13
US-10-311-455-986/c
; Sequence 986, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPERBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 986
; LENGTH: 7597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-986

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Query Match      2.5%; Score 129.4; DB 15; Length 7597;
Best Local Similarity 45.2%; Pred. No. 7.5e-12;
Matches 594; Conservative 0; Mismatches 716; Indels 5; Gaps 3;

QY 156 TCGAAAAAATGCTATTTTAGTTTATAAATTTATTAAGAAATTTTGTGTTGT 215
Db 1338 TCCCGAATAATATCTCCCAATATACATCTCAACCTCTAAATAAATAAATAA 1279
QY 216 TTAAGCATATGTTTGTAACTTAAATAAATATATGTTTAACTTAAATAAAT 275
Db 1278 ATAAATTAACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 1219
QY 276 GTACACATCAATATCTCGAGCATATCAAAACCGTATTCTAGAGCCGATGCGA 335
Db 1218 ATATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 1159
QY 336 ATAGAAGATAATGATTTTAAATAATCGTATCTCCAAATCAATCACTTAGAAG 395
Db 1158 ATCGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1099
QY 396 TGTAAATCTTTATGCTACATAAATAAATAAATAAATAAATAAATAAATAA 455
Db 1098 ATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1039
QY 456 TATAATGCTTTGACAAAAAATTCGAGTCAAAACCCAGTCAATCAAACTATAAG 515
Db 1038 TTAATAAATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 979
QY 516 ATTGAATCAAACTATAGTCGGATGAGTATTAAATTTCCATTTATGTTTCTAT 575
Db 978 TAAATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 919
QY 576 ACCGGAATAATAGATATTATAGATACCAAAAGTAGATTTGTTGTTATATT 635
Db 918 TAAATTTATACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 859
QY 636 TGGAAATTCATCATATCAGGATCTAAAGTAGTCTCCCTAAATTAATCATGTC 695
Db 858 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 799
QY 696 AAGCTCTATGAATGTTTGAATTTGGAAGTTTATTAATTAATTCGGATCTTT 755
Db 798 TAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 739

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11

ALIGNMENTS

```

RESULT 1
US-09-326-203A-1
; Sequence 1, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Lassner, Mike
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045700/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1942
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-326-203A-1
    
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Alignment Scores:
Pred. No.:      4,71e-296      Length:      1942
Score:          2771.00        Matches:      520
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      100.00%     Indels:        0
DB:               4           Gaps:          0
    
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US-09-623-514A-2 (1-520) x US-09-326-203A-1 (1-1942)

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QY      1 MetAlaIleLeuAspSerAlaGlyValThrValThrGluAsnGlyGlyGlyGluPhe 20
|||||
    
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Db 237 ATGGCGATTTTGGATTCTGCTGGGTTACTACGGTCACGGAGAACGGTGGCGGAGAGTTC 296
Qy 21 ValAspLeuAspArgLeuArgArgArgLysSerArgSerAspSerSerAsnGlyLeuLeu 40
Db 297 GTCGATCTCTGATAGGCTTCGTGCGACGGAATCAGATCGGATCTCTTCTTAACGAGCTTCTT 356
Qy 41 LeuSerGlySerAspAsnAsnSerProSerAspAspValGlyAlaProAlaAspValArg 60
Db 357 CTCCTCTGGTTCGGATATATCTCTCTCGGATGATGTTGGAGCTCCCGCGCGAGTTAGG 416
Qy 61 AspArgIleAspSerValValAsnAspAlaGlnGlyThrAlaAsnLeuAlaGlyAsp 80
Db 417 GATCGGATTCGATTCCTGTTGTTAAACGATGACGCTCAGGGAACAGCCAAATTTGGCCGAGAT 476
Qy 81 AsnAsnGlyGlyGlyAspAsnAsnGlyGlyVArgGlyGlyGlnGlyGluGlyArgGlyAsn 100
Db 477 AATAACGGTGGTGGCGATATATAACGGTGGTGGAGAGCGCGCGAGAGAGAGAGAAC 536
Qy 101 AlaAspAlaThrPheThrThrArgProSerValProAlaHisArgAlaArgGluSer 120
Db 537 GCCGATGCTACGTTTACGATATCGACCGCTCGGTTCCAGCTCATCGGAGGCGAGAGAGAT 596
Qy 121 ProLeuSerSerAspAlaIlePheLysGlnSerHisAlaGlyLeuPheAsnLeuCysVal 140
Db 597 CCACCTTAGCTCCGACGCGATCTTCAACACAGAGCCATGCGGATTAATCAACCTCTGTGTA 656
Qy 141 ValValLeuIleAlaValAsnSerArgLeuIleIleGluAsnLeuMetLysThrGlyTrp 160
Db 657 GTAGTTCTTTATTTGCTGTAAACAGTAGACTCATATCGAAAAATCTTATGAAGTAGTGTGG 716
Qy 161 LeuIleAlaThrAspPheThrPheSerSerArgSerLeuArgAspTrpProLeuPheMet 180
Db 717 TTGATCAGAACCGATTTCTGGTTTATGTTCAAGATCGCTGCGAGATTGCGCGCTTTTCATG 776
Qy 181 CysCysIleSerLeuSerIlePheProLeuAlaIlePheThrValGluLysLeuValLeu 200
Db 777 TGTGTGTATATCCCTTTCCGATCTTCTCTTGGCTGCTTACGGTGGAGAAATTTGGTACTT 836
Qy 201 GlnLysThrIleSerGluProValValIlePheLeuHisIleIleIleThrMetThrGlu 220
Db 837 CAGAAATACATATCAGAACCTGTTGTATCTTCTTCTATATATATATATATATATATATAT 896
Qy 221 ValLeuThrProValThrValThrLeuArgCysAspSerAlaPheLeuSerGlyValThr 240
Db 897 GTTTTGTATCCAGTTTACGCTCAACCTTAAGGTGTGATCTCTGCTTTTATATCAGGTGTCACT 956
Qy 241 LeuMetLeuLeuThrCysIleValThrLeuLysLeuValSerThrAlaHisThrSerThr 260
Db 957 TTGATGCTCTCTCACTTGCATTTGTGTGGCTAAGTTGTTTCTTATGCTCATACTAGCTAT 1016
Qy 261 AspIleArgSerLeuAlaAsnAlaIleAspLysAlaAsnProGluValSerThrThrVal 280
Db 1017 GACATAGATCCCTAGCCATGACGCTGATGATAGGCCAATCCCTGAAGTCTCTTACTAGCTT 1076
Qy 281 SerLeuLysSerLeuAlaThrPheMetValAlaProThrLeuCysThrGlnProSerThr 300
Db 1077 AGCTTGAAGAGCTTGGCATATTTATGTTGCTGCCCTCCACATCTGTTATCAGCCAGTTAT 1136
Qy 301 ProArgSerAlaCysIleArgLysGlyTrpValAlaArgGlnPheAlaLysLeuValIle 320
Db 1137 CCACGTTCTGCATGTATACGGAAGGGTGGGTGGCTCGCTCAATTTGCAAAACCTGGTCATA 1196
Qy 321 PheThrGlyPheMetGlyPheIleIleGluGlnThrIleAsnProIleValArgAsnSer 340
Db 1197 TTCACCGGATTCAGGAGTTTATATATAGAACATATATATATATATATATATATATATATAT 1256
Qy 341 LysHisProLeuLysGlyAspLeuLeuThrAlaIleGluArgValLeuLysLeuSerVal 360
Db 1257 AAGCATCTCTTTGAAAGGCGATCTTCTATATATGCTATTTGAAAGAGTGTGAAGCTTTTCAGTT 1316
Qy 361 ProAsnLeuThrValTrpLeuCysMetPheThrCysPhePheHisLeuTrpLeuAsnIle 380
Db 1317 CCAAATTTAT 1376